DATA EVALUATION RECORD
HONEYBEES FIELD TEST
Apis mellifera
Non-Guideline Semi-Field and Residue Study

1. CHEMICAL: Sulfoxaflor PC Code No.: 005210

2. TEST MATERIAL: GF-2626 (ai: Sulfoxaflor) Purity: 11.8% w/w (125 g ai/L)

3. CITATION

Author: Renz, D.

Title: Brood Development of the Honey Bee (*Apis mellifera* L.) in a Semi-Field Tunnel Study in *Phacelia tanacetifolia* in Germany 2016

Study Completion Date: July 26, 2017

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6. DISCLAIMER: *This Data Evaluation Record may have been altered by the Environmental Fate and Effects Division subsequent to signing by CDM/CSS-Dynamac JV personnel. The CDM/CSS-Dynamac Joint Venture role does not include establishing Agency policies.*

7. STUDY PARAMETERS

Test Species: Honeybees (*Apis mellifera* L.)
Age of Test Organism at Test Initiation: Healthy colonies contained one queen with 5135 to 8060 bees (all ages of honeybees included), 6-9 brood combs with all brood stages, 2-8 honey and pollen combs
Test Duration: Experimental phase from June 30, 2016 to March 28, 2017.

8. CONCLUSIONS: GF-2626 (ai: Sulfoxaflor) was applied at rates of 24 and 48 g ai/ha to flowering plants (*Phacelia tanacetifolia*) in Pforzheim, Germany with one water control. Additionally, two toxic reference control groups were used. The honey bee (*Apis mellifera*) colonies were exposed for 7 days using 6 replicate tunnel tents per treatment level. Three replicate tunnel tents per treatment level were used for the two reference control groups. Following the 7-day exposure and relocation, the hives were monitored until 108 days after application 2 (108DAA2) and again at the end of overwintering. The 24 and 48 g ai/ha treatment groups are referred to as T1 and T2 while the 400 g ai/ha and 300 g ai/ha reference control groups are referred to as Re1 and Re2 by the reviewer in select portions of this DER and in the Conclusions section.

Based on the study author's results and interpretation, the applications of 24 g and 48 g ai/ha resulted in a slight increase in mortality on the day after treatments were applied. No effect on the mortality of worker bee pupae, male adult bees, or male pupae was observed. Foraging activity in T1 and T2 decreased on the day of application during bee flight and reduced flight activity was observed at the beginning of the exposure period in the tunnels for T1 and T2. Treatments T1 and T2 influenced the behavior of honeybees, mainly on the day of application during bee flight. There was no effect of treatment T1 or T2 on colony size, total number of brood cells, storage of nectar and pollen, brood index, compensation index, termination rate of eggs/young larvae/old larvae, or pupae weight.

REVIEWER'S CONSIDERATION OF STUDY STRENGTHS, LIMITATIONS, AND INTERPRETATION

It is important to recognize the inherent strengths and limitations of this study as results are interpreted and potentially considered in risk assessment.

In the context of available field studies involving honey bees, this study contains some strengths including:

- Inclusion of multiple colony-level endpoints reflecting hive condition, brood development, and nectar/pollen availability.
- Availability of raw data for conducting statistical analysis.
- Quantification of exposure to sulfoxaflor in hive and plant matrices (pollen from traps, pollen and nectar from combs, nectar from foraging bees, Phacelia plants, and brood comb larvae and pupae).
- Detailed QA/QC results regarding quantification of sulfoxaflor residues in various matrices.

Some limitations were noted, including:

- Transit and storage stability of the residue samples were not assessed.

9. ADEQUACY OF THE STUDY: This study **is scientifically sound** and is classified as **acceptable**.

10. GUIDELINE DEVIATIONS: This semi-field study was conducted following OECD guidance document No. 75, OEPP/EPPO guideline 170(4), and EC guidance document 7029/VI/95. One deviation, which did not have an impact on the study, was that the source of bees was not clearly defined by the author.

11. SUBMISSION PURPOSE: This study was conducted to investigate the potential effects of sulfoxaflor exposure to honey bee (*Apis mellifera*) mortality, behavior, foraging activity, colony condition, brood development, colony infestation level, pupae weight and malformations, and residues after application to flowering plants (*Phacelia tanacetifolia*).

12. MATERIALS AND METHODS

Test Material:

Identity:	GF-2626
IUPAC name (ai):	Not reported
CAS name (ai):	Not reported

CAS No.:	None for formulation (946578-00-3 for Sulfoxaflor)
Lot No.:	ENBK-143945-007A
Description:	Liquid, off-white to tan
Purity:	11.8%, 125 g ai/L (analyzed)
Storage:	Ambient (≤ +30 °C), dark, dry

Test Organisms/Hives: The honeybees (*Apis mellifera* L.) used in the test were from colonies that contained 10 combs each and a sister queen that originated from one breeding line. The test colonies were as homogeneous as possible and contained 5135 to 8060 honey bees at study start. Colonies were free of symptoms of nosemosis, varroosis, foulbrood and other bee diseases. At the start of the test, the colonies were queen-right, contained all brood stages (eggs, larvae, and capped cells), and contained honey and pollen stores. For dead bee assessments, wooden dead bee traps with gauze on the bottom and on the top were attached to the entrance of the colonies.

Test Design: The semi-field test location was near Pforzheim in Baden-Württemberg, Germany and conducted in a field covered with *Phacelia tanacetifolia*. Twenty-nine tunnels were set-up prior to the flowering of plants and prior to moving hives to the experimental field location. Each tunnel covered an area of 100 m^2, had a height of 3.5 m, and was 20 m^2 in length except T1s, T2s, and Cs which had a covered area of 200 m^2 and a length of 40 m^2. The treated crop area covered 82.72 m^2 and the distance between tunnels was 3 m. Each tunnel frame was covered with a light plastic gauze with a 1.5 mm mesh size. A container filled with water was provided to each tunnel and the surface was covered with a floatable material to prevent bees from drowning. Prior to testing onset, paths were created in the middle and at both ends of each tunnel by removing plants and smoothing the ground.

Four days prior to test applications and at the onset of *Phacelia* flowering, one small commercial bee colony was introduced to each tunnel. Installation was carried out in the evening after daily bee flight on July 4, 2016. The 7-day exposure was conducted in the tunnel tents, and the then the hives were relocated to a monitoring site until 40 days after application 2(40DAA2). The monitoring site was located approximately 3 km from the field testing site.

Nominal application rates/volumes: The nominal GF-2626 (ai: Sulfoxaflor) application rates were 0 (negative tap water control), 24, and 48 g ai/ha for the test item (equivalent to 192 mL and 384 mL product/ha). The first reference item, Perfekthion was tested at 400 g ai/ha (1000 mL product/ha) and the second reference item, Insegar (25.1% fenoxycarb), was tested at 300 g ai/ha (1200 g product/ha). The target spray volume was 400 L/ha for all applications.

Application Procedure: The test item solution was prepared shortly before the

application and applied using a calibrated portable boom sprayer simulating a commercial application. Treatment applications were performed during daily bee flight activity on full flowering *P. tanacetifolia* plants (BBCH 63-64) in the replicate treatment tunnels. During all applications, bees were actively foraging (≥10 honey bees/ m^2 per treatment group), wind speed did not exceed 2 m/s, air temperature did not exceed 30°C or drop below 11.4°C, and mean spray tolerance was ±10% per treatment group. During the applications, honey bee colonies in the tunnels were covered with plastic sheets and the water supply was moved out of the tunnels until the end of application to avoid direct contamination. The amount of control, test item, or reference item solution applied was determined by measuring the initial and the remaining spray solution.

Observations: Meteorological data including air temperature, humidity, wind speed, and cloud cover were measured directly with field equipment (GLP record).

Mortality was determined daily by counting the number of dead honey bees in the dead bee traps in front of the hives, on the bottom drawer inside the hives and on the linen sheets which were spread out in the tunnels (exposure period in the tunnels only; there were no linen sheets at the monitoring site). The daily mortality assessments started 3 days before application (3DBA), on the day before application (once before application in T1 and T2), on the day of application before application occurred, after application at 2, 4, and 6 hours, and in evening after flight activity), daily from 1DAA2 to 7DAA2 between morning and noon, and daily for up to 40 days after application (40DAA) in between morning and noon. The bee colonies were removed from tunnel tents on 8DAA and brought to a monitoring site for further mortality assessments up to 40DAA. For the 8DAA to 40DAA interval, only the dead bee traps and bottom drawer were used for mortality assessments. The dead bees found were differentiated into adult worker bees, pupae, and larvae during each assessment, and the exact number of each was recorded. Dead male bees and male brood were also recorded and evaluated. Dead bees were removed after each assessment. Assessments were carried out in the replicates intended for biological observations (replicates a-f) but not for replicates intended for sampling only (Cs, T1s, T2s, Re1s, Re2s). For the calculation of mean mortality values and standard deviations, the numbers of dead honey bees on the linen sheets, if applicable, were added to the dead honey bees in the dead bee traps and on the bottom drawers recorded during the same assessment, and counted as one value.

For foraging activity assessments, the bees were observed daily the 3 days before application (3DBA2), 1 day before application (1DBA2) in T1 and T2, once shortly before application (0DBA2), on the day of application (0DAA2) (twice during the first hour after application, then 2, 4, and 6 hours after), on 1DAA2 (three times during flight activity), and once daily up to 7DAA2. At each assessment time, the number of bees that were both foraging on flowers in the assessments areas or flying over the crop were counted on three foraging assessment areas of 1 m^2 per tunnel (number of forager honey

bees/m^2 flowering *Phacelia tanacetifolia*) for one minute. The location of the assessment areas was chosen randomly prior to each assessment.

Behavior during the study was assessed daily at the same time as mortality and foraging activity. The possible abnormal symptoms compared to the control bees included: intensive cleaning, trembling, cramping, locomotion problems, inactive bees, filtering bees, flying without landing on the crop, hanging bees, and clustering at the hive entrance.

The colony condition assessments were conducted before installation of the colonies at the test site (8DBA2), 2DBA2, 3 days after the application (3DAA2), and 10 times at the monitoring site on 8DAA2, 14DAA2, 20DAA2, 24DAA2, 31DAA2, 35DAA2, 54DAA2, 69DAA2, 82DAA2, 98DAA2, 108DAA2, and at the end of overwintering. The colony condition assessments determined colony strength (number of bees), presence of a healthy queen, comb areas containing brood (eggs, larvae, and capped cells), and comb areas with food stores (pollen, nectar, and honey). The percentage areas covered were estimated and mean values were calculated based on estimates. At each colony assessment, colonies were assessed for bee diseases by a beekeeper according to standard beekeeping practice.

The development of the bee brood was assessed in individually marked brood cells over two independent brood cycles. At the assessment before application (2DBA2 = BFD0 of the 1st brood cycle) and at the assessment on 14DAA2 (= BFD0 of the 2nd brood cycle) one or several brood combs were taken out of each colony to mark areas containing at least 200 eggs, 200 young larvae and 200 old larvae on the comb(s). The selected combs were uniquely identified. The fixed brood areas were photographed during each brood stage assessment (photographic assessments) and the digital photos were transferred to a computer for analysis (Hive Analyzer® software). The same marked cells were assessed for each assessment to determine cell development throughout the study. The pre-imaginal development period of worker honey bee from egg to hatched bee typically averages 21 days. The time schedule of the brood stage assessments was chosen to observe the bee brood at different stages during this period until the expected completion of development. Photographic assessments were not conducted during adverse weather conditions which might have affected the colonies. The brood index, compensation index, and brood termination rate were determined from the marked brood cells.

Honeybee pupae were collected from the combs of the hives intended for biological evaluations (replicates a-f in C, T1, T2, Re1 and Re2) once during the study for weighing and determination of abnormalities. Pupae were collected only from those combs which had not been selected and marked for brood comb photography during the 1st or 2nd brood cycle. On 32DAA2, 30 pupae were collected out of capped cells of brood combs of each hive. Caps were opened, and pupae were gently taken out of the cells using

tweezers. No retained specimens were taken. Samples were kept at ambient conditions in separate sampling boxes per hive and transported to the test facility. All pupae were weighed and checked for abnormalities on the same day and disposed of after completion of the assessment.

Treatment against *Varroa* mites was carried out by evaporation of formic acid in the hives starting August 22, 2016 (45DAA2 = 0DAT; DAT= Days after start of treatment against *Varroa* mites) during a period of good weather. During the treatment and evaluation period, the hive floor was equipped with a solid board covered with sticky cloth to trap also those fallen mites that were still alive. Mites on the floor of each hive were counted on 28DAT. The mites were removed, and the sticky cloth was renewed after each counting.

Sampling:
Forager bees were sampled from hive entrances Cs, T1s, T2s, Re1s, and Re2s once before and three times after application. Whole *Phacelia* plants were sampled from the same hive entrances twice before application, on the day of application, and six times after application. Plants were pooled per sub-sample and replicate (12 plants for sub-sample A and B). Pollen from pollen traps were sampled from hive entrances Cs, T1s, T2s, Re1s, and Re2s once before and six times after application. The grid of the pollen trap was inserted during time of honeybee foraging activity and kept in place for approximately 4 hours.

Pollen from combs was sampled with a pollen extractor and nectar from combs with a syringe on 7DAA2. Samples were taken only from colonies Cs, T1s, T2s, Re1s and Re2s. Pre-pupal worker larvae (5th instar) and worker pupae (from capped brood cells) were sampled with a small spatula on 7DAA2. Samples were taken only from colonies Cs, T1s, T2s, Re1s and Re2s. The nectar of approx. 50 forager bees was taken to determine the sugar content of the nectar. Sugar content was determined by using a digital refractometer. The *Phacelia* plants samples, pollen from trap samples, nectar and pollen from comb samples, larvae and pupae from brood comb samples and the honey stomach contents and pollen loads (from forager bees, after preparation) were transferred in deep frozen condition to the Principal Investigator for residue analysis (Eurofins Agroscience Services EcoChem GmbH / Eurofins Agroscience Services Ecotox GmbH).

For all sampling procedures, samples were split into two sub-samples (A for analysis and R to be retained), each sub-sample was labelled uniquely, and samples were stored deep frozen after the end of sampling then maintained until start of the analysis.

Residue Analysis Method: All residue analyses were conducted at Eurofins Agrosciences EcoChem GmbH / Eurofins Agroscience Services Ecotox GmbH.

Residues of sulfoxaflor were determined in samples of whole *Phacelia* plants, pollen and nectar from comb, pollen from trap, larvae from comb, and pupae from brood comb and nectar.

Quantification was performed using LC-MS/MS. The LOQ was 0.01 mg/kg and the LOD was 0.003 mg/kg for each matrix.

Statistical Analysis: The statistical analysis of mortality (except male bee mortality), foraging activity data, colony data (number of bees, food cells, and brood cells), and the brood termination rates, brood indices and compensation indices resulting from the photographic assessments, pupae weights, and total number of fallen *Varroa* mites were conducted using SAS software (version 9.3). No statistical evaluation of dead male bees and male pupae was carried out due to their rare occurrence during this study and the low informative value of those records. For all tests, the significance level was set as $\alpha = 0.05$. For the pre-application period, all tests were conducted in a two-sided approach. For data assessed after application, one-sided tests were conducted ("upper" for mortality data and brood termination rates, "lower" for flight activity, *Varroa* counts, brood index, compensation index, pupae weights, and colony assessment data). For evaluation of mortality, the number dead bees on the linen sheets, in the dead bee traps, and on the hive floor (bottom drawer) were summarized per replicate. Data of the treatment groups and the control were checked for normality using Shapiro-Wilks test. If the distribution of the data fitted the normal distribution very well (Shapiro-Wilks test, $p \geq 0.2$), then Bartlett's test was used to check for homoscedasticity of data or in the other cases Levene's test was used. If logarithmic transformation of data solved problems with normality or homoscedasticity transformed data were used for analysis to enable use of tests with higher statistical power. If normality and homoscedasticity were proven, Dunnett's t-test was used for analysis of the data. If normality was met but homoscedasticity was disturbed, the Bonferroni-Holms corrected Satterthwaite t-test (same as Welch test) was used for analysis. If data were not normal, the Bonferroni-Holms corrected U-test was used.

Summary of Study Dates:

Chronological list of activities[a]:

Week	Date	Activity
8DBA2/7DBA2	30 Jun/01 Jul 2016	Pre-colony assessment of all colonies (replicates a-f and s for C, T1, T2 and replicates a-c and s for Re1 and Re2)
4DBA2	04 July 2016	Installation of honeybee colonies inside the tunnel tents (in the evening)
3DBA2	05 July 2016	First assessments of mortality and foraging activity and behavior in the tunnel
2DBA2 /	06 July 2016	Photographic assessment (BFD) and 1st colony assessment

Week	Date	Activity
BFD0 (1st cycle)		
1DBA2	07 July 2016	1st Sampling of forager bees, pollen from trap and plants (Cs, T1s, T2s, Re1s and Re2s) and sampling of plants in all tunnels
1DBA2/0DBA2	07/08 July 2016	Application of test item groups T1 and T2 (after bee flight)
0DAA2 (BBCH 65)	08 July 2016	Application of tap water (control) and reference items (Re1 and Re2) during honeybee flight
0DAA2	08 July 2016	2nd Sampling of forager bees, pollen from trap and plants (Cs, T1s, T2s, Re1s and Re2s) and sampling plants in all tunnels
1DAA2	09 July 2016	3rd Sampling of forager bees, pollen from trap and plants (Cs, T1s, T2s, Re1s and Re2s)
2DAA2	10 July 2016	4th Sampling of forager bees, pollen from trap and plants (Cs, T1s and T2s)
3DAA2 / BFD+5 (1st cycle)	11 Jul 2016	2nd photographic assessment and 2nd colony assessment
3DAA2	11 Jul 2016	5th Sampling of forager bees, pollen from trap and plants (Cs, T1s and T2s)
4DAA2	12 Jul 2016	6th Sampling of forager bees, pollen from trap and plants (Cs, T1s and T2s)
7DAA2	15 Jul 2016	7th Sampling of forager bees, pollen from trap, plants, nectar and pollen from comb, larvae and pupae from comb (Cs, T1s, T2s, Re1s and Re2s)
7DAA2	15 Jul 2016	Relocation of hives to the monitoring site (in the evening after daily honeybee-flight)
7DAA2	15 Jul 2016	First assessment of mortality and behavior at monitoring site
8DAA2	16 Jul 2016	4th Feeding (2 L)
8DAA2 / BFD+10 (1st cycle)	16 Jul 2016	3rd photographic assessment and 3rd colony assessment
14DAA2 / BFD+16 (1st cycle) / BFD0 (2nd cycle)	22 Jul 2016	4th photographic assessment and 4th colony assessment; selection of brood cells for 2nd brood cycle
20DAA2 / BFD+22 (1st cycle) / BFD+6 (2nd cycle)	28 Jul 2016	5th photographic assessment and 5th colony assessment
24DAA2 / BFD+10 (2nd cycle)	01 Aug 2016	6th photographic assessment and 6th colony assessment
31DAA2 /	08 Aug 2016	7th photographic assessment and 7th colony assessment

Week	Date	Activity
BFD+17 (2nd cycle)		
32DAA2 / BFD+18	09 Aug 2016	Sampling of pupae from combs in all biological hives
35DAA2 / BFD+21 (2nd cycle)	12 Aug 2016	8th photographic assessment and 8th colony assessment
40DAA2	17 Aug 2016	Last assessment of mortality and behavior at monitoring site
45DAA2	22 Aug 2016	1st treatment against *Varroa*
54DAA2	31 Aug 2016	9th colony assessment and beekeeper check
69DAA2	15 Sep 2016	10th colony assessment
73DAA2 (28DAT)	19 Sep 2016	Counting of *Varroa* mites
74DAA2	20 Sep 2016	2nd treatment against *Varroa*
82DAA2	28 Sep 2016	Beekeeper Check
98DAA2	14 Oct 2016	11th colony assessment
108DAA2	24 Oct 2016	Beekeeper Check
End of overwintering	28 Mar 2017	12th colony assessment

[a] DBA2 = Days before application A2; DAA2 = Days after application A2; BFD = Brood fixing day; DAT = days after start of treatment against *Varroa*

13. REVIEWERS RESULTS

Statistics. For the reviewer calculated results statistics were run using R programing (R Core Team 2013). As the data permitted comparisons were run between control and treatment groups as outlined in Appendix A. Where appropriate Dunnets test or Wilcoxen tests were used for these comparisons.

Adult Mortality. Adult foraging bees exposed to GF-2626 at rates of 24 and 48 g a.i./ha (during flight) exhibited a statistically-significant increases in mortality of up to 5.5X the rate observed in controls on the day of application. This increase in mean daily worker bee mortality was short lived, however, having returned to not significantly increased 1DAA (for the 24 and 48 g a.i./ha treatments). No statistically significant increases in daily mortality rates were detected after 0DAA.

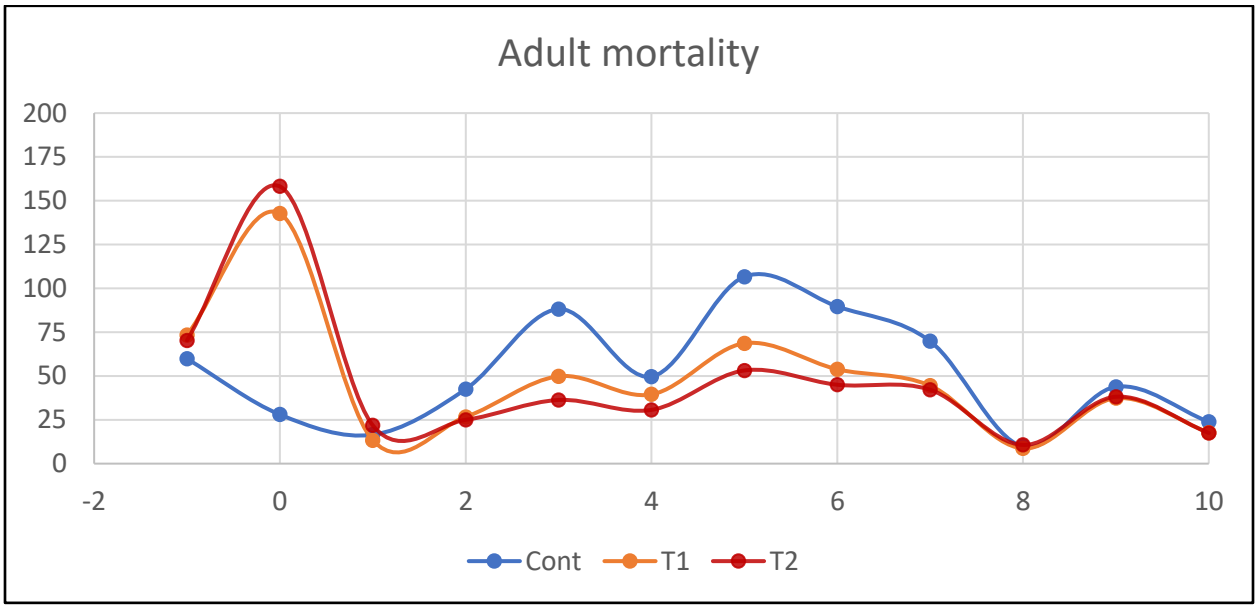

Figure 1. Mortality of adults bees per day.

Foraging Intensity. Application of GF-2032 led to a reduction of foraging activity of bees on the day of application. However, immediately prior to application foraging activity was significantly reduced in both treatment groups. Relative to control bees, mean foraging intensity on 0DAA was reduced by 50% in the 24 and 48 g a.i./ha treatment groups. For the remainder of the test, mean forage intensity of bees was decreased in both treatment groups but should be interpreted with caution as flight activity was reduced before application at similar levels.

Behavioral Effects. On the day following application for treatment 1, there were 86 bees with locomotion issues, 24 cramping bees, and 2 flying without landing bees. For treatment 2, there were 51 bees with locomotion problems, 4 trembling, and 39 cramping. During the further exposure period (1DAA2 to 7DAA2) there were 12 bees exhibiting abnormal behavior. When compared to the control, treatments 1 and 2 generally resulted in more abnormal behaviors and can be said to influence the behavior of worker bees, but these effects diminished rapidly.

Colony Strength. The effect of sulfoxaflor on colony strength is difficult to interpret due to large variation between hives. There were no sustained effects to colony strength at any timepoint. There were no obvious dose-dependent trends in colony strength apparent among hives. Number of cells with eggs was significantly different from control at 20DAA. While number of cells with larvae was significantly different from control at 35DAA and 69DAA. These differences were not sustained in between these timepoints.

Brood Condition. Brood indices, compensation indices, and termination rates of eggs, young larvae and old larvae in T1 and T2 of the first and second brood cycle were not significantly different from the control. There was high brood termination in the first cycle analyzed, which is often an artifact of the hive being constrained in the tunnel system. The brood termination rate was not different between controls and treatments and had recovered by the second brood cycle analyzed.

Residues. Residues of sulfoxaflor in nectar collected by bees peaked the day of application (0.35mg/kg) and declined with application rate and over time until no longer detected at day 3DAA. Residues in bee collected pollen up to 1 mg/kg were detected the day of application and declined with application rate and over time until day 7DAA. Residues in plants (max of 0.56 mg/kg on 0DAA) declined steadily in the 24 and 48 g ai/ha treated plots to about 0.02 mg/kg by 7DAA.

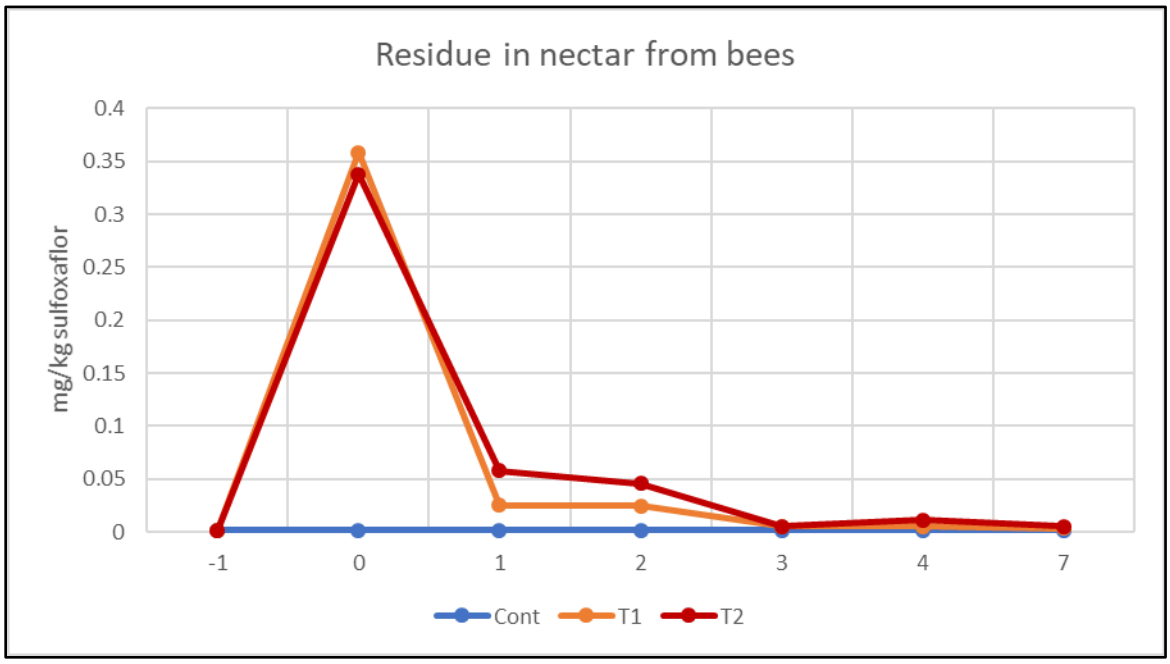

Figure 2. Sulfoxaflor residues in bee-collected nectar per day.

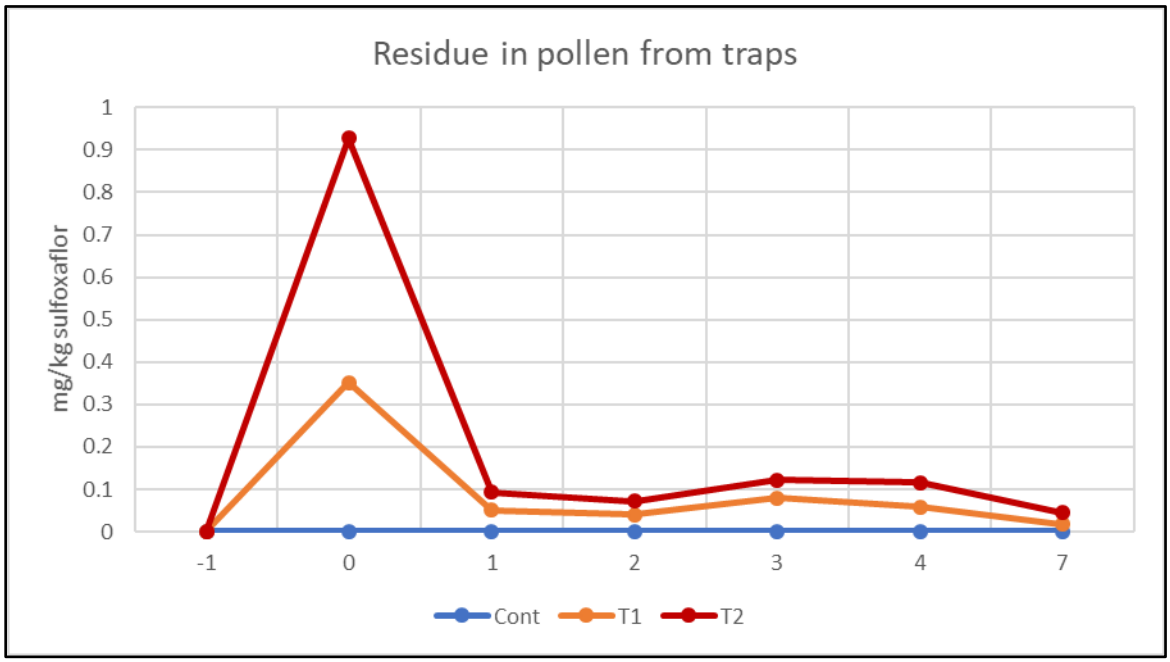

Figure 3. Sulfoxaflor residues in pollen collected from traps per day.

DT_{50}. In this study, separate trials (tunnels) were evaluated with two different foliar spray application rates during bloom (0.022 and 0.042 lb a.i./A). Among both matrices, DT_{50} values varied from 0.29 days (nectar) to 1.5 days (nectar/pollen), indicating relatively rapid decline of sulfoxaflor in bee-relevant matrices. These DT_{50} values indicate that repeated application of sulfoxaflor would not lead to additional accumulation in pollen and nectar (*e.g.,* no or negligible carry over) with the proposed minimum 7-d retreatment interval. Output from the modeling to calculate these values is reported in Appendix B.

DT_{50} and DT_{90} values for sulfoxaflor in buckwheat matrices

Crop (Region)	DT_{50} Values	DT_{90} Values
Nectar from Bees		
Phacelia (Germany)	0.29-0.45	0.95-1.5
Pollen from Traps		
Phacelia (Germany)	0.33-0.45	1.1-1.5

Overwintering. All hives from this study survived overwintering with no effects observed at any treatment level.

14. STUDY AUTHOR REPORTED RESULTS

Mortality: For treatment 1 (T1), mean mortality after application rose to 192.5 dead bees/colony for the day after first exposure compared to the mean mortality of the pre-exposure period of 54.6. This was also statistically higher than the mean dead bees/colony in the control (47.2). During the monitoring period (8DAA2 to 40DAA2), mean mortality was comparable to the corresponding control group at 29.1 dead bees/colony. Mortality rose to 281.2 dead bees/colony on the day of application during bee flight from its pre-exposure mortality of 64.6 in treatment 2 (T2). This was significantly different from the control group (47.2). During the monitoring period, mean mortality was 20.7 bees/colony.

Concerning mortality of larvae and pupae, there were 0.4 dead larvae + pupae/colony during the pre-exposure period for treatment T1. On the day of application (A2), the mean mortality rose to 1.2 dead larvae + pupae/colony. During the exposure period (0DBA2 to 7DAA2), mean mortality in the T1 tunnel was 4.4 larvae + pupae/colony as compared to 4.8 larvae + pupae/colony in the control. For the monitoring period (8DAA2 to 40DAA2) there was a noticeable drop in mortality to 1.0 larvae + pupae/colony which was comparable to the control group (1.3). For treatment 2 (T2), mean mortality on the day of application was 0.0 and rose to 3.5 dead larvae + pupae/colony during the exposure period. However, this number fell during the monitoring period to 0.7 which was lower than the mean mortality noted for the control group.

Mortality of male bees, male larvae, and male pupae was also measured. For treatment 1 (T1), the mean mortality during the pre-exposure period was 0.9 dead males/colony and 0.2 dead male larvae + pupae/colony. On the day of application during bee flight, mortality rose to 2.2 dead males/colony and 0.5 dead male larvae + pupae/colony. Dead males/colony decreased to 1.0 and dead male larvae increased to 1.3 during the exposure period before both ultimately dropped to 0.3 and 0.1 during the monitoring period, respectively. Regarding treatment 2 (T2), mortality began higher in the pre-exposure period and dropped on the day of application. During the actual exposure period, there were 2.1 dead males/colony and 1.0 dead male larvae + pupae/colony. However, in the monitoring period, mean mortality decreased to 0.4 dead males/colony and 0.0 dead male larvae + pupae/colony.

Foraging Activity: Concerning application after bee flight (A1, relevant for T1 and T2), the mean pre-application flight intensity (3DBA2 to 1DBA2) was 17.3 forager bees/m^2/min compared to 20.5 forager bees/m^2/min in the post-application period (0DBA2 to 7DAA2). Mean flight intensity on the day of application during bee flight (0DBA2 to 0DAA2) was 30.6 forager bees/m^2/min. For the application during bee flight (A2), the mean pre-application flight intensity was 20.4 forager bees/m^2/min compared to 20.5 forager bees/m^2/min in the post application period. Regarding treatment 1 (T1),

mean foraging activity on 0DBA2 to 0DAA2 was significantly lower when compared to the control. Similarly, mean foraging activity during the entire exposure period was also significantly lower than the control. For treatment 2 (T2), mean foraging activity on 0DBA2 to 0DAA2 was also significantly lower when compared to the control. Additionally, significant differences in foraging activity were observed on 1DAA2, 2DAA2, 6DAA2, and 7DAA2.

Behavior: No unusual behaviors were observed during the pre-application period (3DBA2 to 1DBA2) except for one bee with locomotion issues in Ca. In the post application period (0DAA2 to 7DAA2) in treatment T1, there were 4 bees with locomotion problems in the control. On the day following application A1 (0DBA2/0DAA2), there were 86 bees with locomotion issues, 24 cramping bees, and 2 flying without landing bees. In the exposure period, 5 bees had locomotion problems, 4 were inactive, and 1 was cramping. For treatment 2 (T2) on 0DBA2/0DAA2, there were 51 bees with locomotion problems, 4 trembling, and 39 cramping. During the further exposure period (1DAA2 to 7DAA2) there were 3 cramping bees, 6 inactive, 1 hanging, and 2 exhibiting excessive cleaning. At the monitoring site (8DAA2 to 40 DAA2), behavioral abnormalities were dominated by locomotion problems, which amounted to 15, 43, and 55 bees in the control, T1, and T2 groups, respectively. When compared to the control, treatments 1 and 2 generally resulted in more abnormal behaviors (more cramping, locomotion issues, trembling) and can be said to influence the behavior of worker bees.

Colony Condition: On 8DBA2 the mean colony size (number of honeybees/colony) was not significantly different between all treatment groups with 6858 in C, 7291 in T1, 7193 in T2, 7280 in Re1, and 7128 in Re2. Mean colony sizes grew slightly in C, T2, and Re2 during the exposure period in the tunnels (3DAA2) but there was a slight decrease in colony size observed for T1. After relocation, the mean colony sizes were 12231 bees/colony in C, 10660 in T1, and 11018 in T2 on 8DAA2. There were no statistically significant differences between T1 and T2 compared to C on any day from 8DBA2 until assessment after overwintering.

Amount of Brood: Brood of all stages (eggs, larvae, pupae) was present in all colonies at all assessment dates from 8DBA2 to 54DAA2 except the intermittent lack of larvae in hives Ca, Cc, Cf, T1b, T1d, and T1f on three different days after application 2 (3, 8, and 54). No eggs were observed on 54DAA2 for T1f and no pupae were observed on 14DAA2 in T1b. During the final two assessments before overwintering, certain brood stages were missing or on a very low level in several hives of all treatment groups including the control. The total number of brood cells of all stages per colony was 30033 in C, 30033 in T1, and 29967 in T2 at the start of the study (8DBA2). Although minor increases were observed until 2DBA2, none were statistically different from the control. In the post-application exposure period and the following two assessments after

relocation, the total amount of brood decreased in all treatments. After moderate feeding on 14DAA2, the amount of brood increased during the following two assessments and reached its post-exposure maximum of 21533 brood cells per colony in C, 20000 in T1, and 22700 in T2. A slow decrease in number of brood cells was observed in all treatments including the control on 31DAA2, 35DAA2, and 54DAA2. By 98DAA2, the number of eggs and larvae had reached very low values in all treatments and controls. Overall, there was no effect of exposure in T1 or T2 on brood or particular brood stages during the post-exposure period.

Amount of Nectar: The mean number of nectar cells/colony was similar in all treatment groups at 8DBA2: 7767 in C, 7833 in T1, and 7100 in T2. To prevent starvation, moderate feeding of all hives was done on 14DAA2. After feeding, there were no significantly different values regarding the amount of nectar observed between treatments and the control. In preparation for the first treatment of the hives for Varroa mites, all hives were fed 10 kg sucrose solution on 35DAA2. Additionally, intensive feeding of all colonies was performed on 63DAA2 to prepare the colonies for overwintering. There were no significant differences observed between the control and treatments during the entire study.

Amount of Pollen: The mean amount of pollen per hive was similar in all treatments before installation of the colonies into tunnels except for a significantly greater amount of pollen in T2. Pollen was available at all assessments during the study period except for a temporary lack of pollen in Ca on 8DBA2, Cb on 8DAA2 and 14DAA2, T1b on 14DAA2, and in T1c on 35DAA2. For treatments T1 and T2, there were no significant differences of the pollen supply compared to the control except one record of reduced amounts of pollen in T1 on 24DAA2. However, this one incident was likely due to seasonal scarcity of natural pollen sources and was not considered treatment related. Overall, there was no treatment related effect on pollen storage in treatments T1 or T2.

Brood Development: Brood indices, compensation indices, and termination rates of eggs, young larvae and old larvae in T1 and T2 of the first and second brood cycle were not significantly different from the control.

Weight Determination and Morphological Assessment of Pupae: Mean pupae weights were not significantly different from the control at 0.1372 g in the control, 0.1349 g in T1, and 0.1351 g in T2. No malformations were observed in all treatments (including Re1 and Re2) and the control.

Counting of *Varroa* mites after anti-*Varroa* treatment: Mean mites/day in all treatment groups were not significantly different from the control.

Analytical Results: In the untreated and control samples, there were no residues of

sulfoxaflor at or above the limit of quantification (LOQ) levels (0.01 mg sulfoxaflor/kg) in any of the untreated samples taken from the control at any sampling date or in samples from T1 or T2 that were collected on 1DBA2. Sulfoxaflor residues (mg/kg) in pollen from traps began at 0.351 but trended downward by 7DAA2 to 0.0179 for T1. A similar trend was observed for T2, which started at 0.928 on 0DAA2 but decreased to 0.0452 at 7DAA2. No residues were detected in the pollen from combs in T1 but residues of 0.0615 mg/kg were detected in T2. In the nectar from combs, sulfoxaflor residues were 0.0181 mg/kg in T1 and 0.0466 mg/kg in T2. Regarding the nectar from forager bees, residues were at 0.359 mg/kg initially in T1 and decreased to <LOQ by 7DAA2. For T2, residues were as high as 0.338 mg/kg on 0DAA2 and fell to <LOQ by 7DAA2. Residues on *Phacelia tanacetifolia* in T1 began at a mean of 0.467 mg/kg at 0DAA2 and dropped to a mean of 0.0201 mg/kg by 7DAA2. A similar trend was observed for T2, which began at a mean of 0.564 mg/kg and fell to 0.0213 mg/kg by 7DAA2. To note, the highest level of sulfoxaflor residues were observed in *Phacelia* in T2. In the larvae from brood combs, sulfoxaflor residues were 0.00619 mg/kg for T1 and 0.0104 mg/kg for T2. No residues in pupae from brood combs were detected at or above the LOD in T1 and T2.

Table 1. Mean (min, max) sulfoxaflor concentrations in nectar from bees, nectar from combs, pollen from traps, pollen from combs, and plants.

DAA	Control	Treatment 1	Treatment 2
Nectar from Bees			
-1	<LOD	<LOD	<LOD
0	<LOD	0.359	0.338
1	<LOD	0.0253	0.0581
2	<LOD	0.0244	0.0460
3	<LOD	<LOQ	<LOQ
4	<LOD	<LOQ	0.0116
7	<LOD	<LOQ	<LOQ
Nectar from Combs			
7	<LOD	0.0181	0.0466
Pollen from Traps			
-1	<LOD	<LOD	<LOD
0	<LOD	0.351	0.928
1	<LOD	0.0503	0.0938
2	<LOD	0.0409	0.072
3	<LOD	0.0795	0.122
4	<LOD	0.0583	0.117
7	<LOD	0.0179	0.0452
Pollen from Combs			
7	<LOD	<LOD	0.0615
Plants			
-1	<LOD (<LOD, <LOD)	<LOD (<LOD, <LOD)	<LOD (<LOD, <LOD)
0	<LOD	0.467 (0.159, 0.745)	0.564 (0.357-1.00)

1	<LOD	0.234	0.273
2	<LOD	0.156	0.272
3	<LOD	0.0990	0.147
4	<LOD	0.110	0.145
7	<LOD	0.0201	0.0213

LOQ = 0.01 mg/kg for all matrices.
LOD = 0.003 mg/kg for all matrices.
Replicate data were calculated by averaging the A and B subsamples for each discrete sampling interval.

15. REVIEWER'S CONSIDERATION OF STUDY STRENGTHS, LIMITATIONS, AND INTERPRETATION

It is important to recognize the inherent strengths and limitations of this study as results are interpreted and potentially considered in risk assessment.

In the context of available field studies involving honey bees, this study contains some strengths including:

- Inclusion of multiple colony-level endpoints reflecting hive condition, brood development, and nectar/pollen availability.
- Availability of raw data for conducting statistical analysis.
- Quantification of exposure to sulfoxaflor in hive and plant matrices (pollen from traps, pollen and nectar from combs, nectar from foraging bees, Phacelia plants, and brood comb larvae and pupae).
- Detailed QA/QC results regarding quantification of sulfoxaflor residues in various matrices.

A number of limitations were noted, including:

- Relatively low number of replicates in the treatment and control groups (n = 6).
- Only one application method was tested to determine magnitude and decline kinetics of residues in the various matrices.
- Transit and storage stability of the residue samples were not assessed.

16. REVIEWER'S COMMENTS

Preliminary non-GLP assessments of hives took place from June 30-July 1 2016. Study initiation took place May 19, 2016. The start of the experimental phase was June 30, 2016. The end of the experimental phase was March 28, 2017. Study completion date was July 26, 2017.

Signed and Dated No Data Confidentiality, GLP, and Quality Assurance statements were provided. This study was conducted in accordance the OECD principles of Good Laboratory Practice and respective national regulations.

No reference item was tested.

17. REFERENCES

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IMDORF, A. & GERIG, L. (1999): Lehrgang zur Erfassung der Volksstärke, Schweizerisches Zentrum für Bienenforschung. [Course in Determination of Colony Strength, Swiss Bee Research Center].

IMDORF, A.; BUEHLMANN, G.; GERIG, L.; KILCHMANN, V. AND WILLE, H. (1987): Überprüfung der Schätzmethode zur Ermittlung der Brutfläche und der Anzahl Arbeiterinnen in freifliegenden Bienenvölkern, Apidologie 18 (2), 137 – 146. [A Verification of the Method for Estimation of Brood Areas and Number of Worker Bees in Free-Flying Bee Colonies].

PISTORIUS, J.; BECKER, R.; LÜCKMANN, J.; SCHUR, A.; BARTH, M.; JEKER, L.; SCHMITZER, S.; VON DER OHE, W. (2012): Effectiveness of method improvements to reduce variability of brood termination rate in honey bee brood studies under semi-field conditions. Julius-Kühn-Archiv, 437, 115-120.

All other references are standard guidelines and methodologies.

APPENDIX A

```
R version 3.5.2 (2018-12-20) -- "Eggshell Igloo"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
```

```
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Workspace loaded from ~/.RData]

library("dplyr")
library("ggpubr")
Tunnel1 <-
read.csv(file='C:/Users/mniesen/Documents/Rwork/Tunnel/EUTunnel.
csv', header=TRUE)
Mort1<-
read.csv(file='C:/Users/mniesen/Documents/Rwork/Tunnel/EUMortali
ty.csv', header=TRUE)

> with(Tunnel1, tapply(Adults, Day, shapiro.test))
$`14DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.86013, p-value = 0.01228


$`20DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.89765, p-value = 0.05229


$`24DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93628, p-value = 0.2501


$`2DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.9342, p-value = 0.23


$`31DAA`
```

```
        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.89882, p-value = 0.0548


$`35DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.91654, p-value = 0.1123


$`3DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96282, p-value = 0.657


$`54DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97998, p-value = 0.9498


$`69DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96383, p-value = 0.6768


$`8DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96681, p-value = 0.7361


$`8DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
```

```
W = 0.86836, p-value = 0.01672


$`98DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96737, p-value = 0.747


$OVRW

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.91715, p-value = 0.1151


> with(Tunnel1, tapply(Eggs, Day, shapiro.test))
$`14DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93788, p-value = 0.2665


$`20DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.9519, p-value = 0.4557


$`24DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.80611, p-value = 0.001855


$`2DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94031, p-value = 0.2933
```

```
$`31DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.87822, p-value = 0.02437


$`35DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.961, p-value = 0.6211


$`3DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96967, p-value = 0.7914


$`54DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97337, p-value = 0.8582


$`69DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.90854, p-value = 0.08108


$`8DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97835, p-value = 0.9314


$`8DBA`
```

```
        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96312, p-value = 0.6629


$`98DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.37305, p-value = 7.572e-08


$OVRW

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.889, p-value = 0.0371


> with(Tunnel1, tapply(Larvae, Day, shapiro.test))
$`14DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.88619, p-value = 0.03322


$`20DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.91401, p-value = 0.1013


$`24DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.92915, p-value = 0.1876


$`2DBA`

        Shapiro-Wilk normality test
```

```
data:  X[[i]]
W = 0.94392, p-value = 0.3378


$`31DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96239, p-value = 0.6483


$`35DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.41086, p-value = 1.477e-07


$`3DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.8555, p-value = 0.01035


$`54DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.87096, p-value = 0.01846


$`69DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93465, p-value = 0.2343


$`8DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.92594, p-value = 0.1647
```

```
$`8DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94586, p-value = 0.3637


$`98DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.68522, p-value = 5.403e-05


$OVRW

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.9049, p-value = 0.06999


> with(Tunnel1, tapply(Pupae, Day, shapiro.test))
$`14DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94418, p-value = 0.3411


$`20DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94579, p-value = 0.3628


$`24DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.89435, p-value = 0.04586


$`2DBA`
```

```
        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96482, p-value = 0.6965


$`31DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97375, p-value = 0.8644


$`35DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.92337, p-value = 0.1483


$`3DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97291, p-value = 0.8504


$`54DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.91633, p-value = 0.1113


$`69DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96304, p-value = 0.6612


$`8DAA`

        Shapiro-Wilk normality test
```

```
data:  X[[i]]
W = 0.97091, p-value = 0.8147


$`8DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94042, p-value = 0.2946


$`98DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93509, p-value = 0.2384


$OVRW

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94637, p-value = 0.3709


> with(Tunnel1, tapply(Brood, Day, shapiro.test))
$`14DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.941, p-value = 0.3014


$`20DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93459, p-value = 0.2337


$`24DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.9478, p-value = 0.3915
```

```
$`2DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.9207, p-value = 0.133


$`31DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96897, p-value = 0.7781


$`35DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96578, p-value = 0.7156


$`3DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96424, p-value = 0.6851


$`54DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94302, p-value = 0.3262


$`69DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97281, p-value = 0.8485


$`8DAA`
```

```
        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96924, p-value = 0.7832


$`8DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97978, p-value = 0.9477


$`98DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.56094, p-value = 2.842e-06


$OVRW

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94641, p-value = 0.3715


> with(Tunnel1, tapply(Nectar, Day, shapiro.test))
$`14DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.98067, p-value = 0.9567


$`20DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97514, p-value = 0.8868


$`24DAA`

        Shapiro-Wilk normality test
```

```
data:  X[[i]]
W = 0.94627, p-value = 0.3695


$`2DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.9571, p-value = 0.5468


$`31DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93571, p-value = 0.2444


$`35DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94257, p-value = 0.3205


$`3DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.95566, p-value = 0.5204


$`54DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.98853, p-value = 0.9971


$`69DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.91738, p-value = 0.1162
```

```
$`8DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96117, p-value = 0.6244


$`8DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96021, p-value = 0.6056


$`98DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97561, p-value = 0.8939


$OVRW

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.81907, p-value = 0.002861


> with(Tunnel1, tapply(Pollen, Day, shapiro.test))
$`14DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.8629, p-value = 0.01362


$`20DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96805, p-value = 0.7603
```

```
$`24DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96, p-value = 0.6016


$`2DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.976, p-value = 0.8998


$`31DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96531, p-value = 0.7062


$`35DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96045, p-value = 0.6103


$`3DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93002, p-value = 0.1943


$`54DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96682, p-value = 0.7362


$`69DAA`

        Shapiro-Wilk normality test
```

```
data:  X[[i]]
W = 0.80814, p-value = 0.001984


$`8DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.91448, p-value = 0.1032


$`8DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.89619, p-value = 0.04933


$`98DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.89335, p-value = 0.04407


$OVRW

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93401, p-value = 0.2283

> bartlett.test(Adults[Day=="14DAA"] ~ Trt[Day=="14DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "14DAA"] by Trt[Day == "14DAA"]
Bartlett's K-squared = 1.229, df = 2, p-value = 0.5409

> bartlett.test(Adults[Day=="20DAA"] ~ Trt[Day=="20DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "20DAA"] by Trt[Day == "20DAA"]
Bartlett's K-squared = 2.7932, df = 2, p-value = 0.2474

> bartlett.test(Adults[Day=="24DAA"] ~ Trt[Day=="24DAA"], Tunnel1)
```

```
        Bartlett test of homogeneity of variances

data:  Adults[Day == "24DAA"] by Trt[Day == "24DAA"]
Bartlett's K-squared = 4.3615, df = 2, p-value = 0.113

> bartlett.test(Adults[Day=="2DBA"] ~ Trt[Day=="2DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "2DBA"] by Trt[Day == "2DBA"]
Bartlett's K-squared = 2.445, df = 2, p-value = 0.2945

> bartlett.test(Adults[Day=="31DAA"] ~ Trt[Day=="31DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "31DAA"] by Trt[Day == "31DAA"]
Bartlett's K-squared = 9.8972, df = 2, p-value = 0.007093

> bartlett.test(Adults[Day=="35DAA"] ~ Trt[Day=="35DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "35DAA"] by Trt[Day == "35DAA"]
Bartlett's K-squared = 1.4673, df = 2, p-value = 0.4802

> bartlett.test(Adults[Day=="3DAA"] ~ Trt[Day=="3DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "3DAA"] by Trt[Day == "3DAA"]
Bartlett's K-squared = 4.8556, df = 2, p-value = 0.08823

> bartlett.test(Adults[Day=="54DAA"] ~ Trt[Day=="54DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "54DAA"] by Trt[Day == "54DAA"]
Bartlett's K-squared = 2.0899, df = 2, p-value = 0.3517

> bartlett.test(Adults[Day=="69DAA"] ~ Trt[Day=="69DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "69DAA"] by Trt[Day == "69DAA"]
Bartlett's K-squared = 0.59235, df = 2, p-value = 0.7437

> bartlett.test(Adults[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel1)

        Bartlett test of homogeneity of variances
```

```
data:  Adults[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 2.9222, df = 2, p-value = 0.232

> bartlett.test(Adults[Day=="8DBA"] ~ Trt[Day=="8DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "8DBA"] by Trt[Day == "8DBA"]
Bartlett's K-squared = 0.45616, df = 2, p-value = 0.7961

> bartlett.test(Adults[Day=="98DAA"] ~ Trt[Day=="98DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "98DAA"] by Trt[Day == "98DAA"]
Bartlett's K-squared = 0.17117, df = 2, p-value = 0.918

> bartlett.test(Adults[Day=="OVRW"] ~ Trt[Day=="OVRW"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Adults[Day == "OVRW"] by Trt[Day == "OVRW"]
Bartlett's K-squared = 1.4303, df = 2, p-value = 0.4891

> bartlett.test(Eggs[Day=="14DAA"] ~ Trt[Day=="14DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "14DAA"] by Trt[Day == "14DAA"]
Bartlett's K-squared = 0.51374, df = 2, p-value = 0.7735

> bartlett.test(Eggs[Day=="20DAA"] ~ Trt[Day=="20DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "20DAA"] by Trt[Day == "20DAA"]
Bartlett's K-squared = 0.1626, df = 2, p-value = 0.9219

> bartlett.test(Eggs[Day=="24DAA"] ~ Trt[Day=="24DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "24DAA"] by Trt[Day == "24DAA"]
Bartlett's K-squared = 3.6459, df = 2, p-value = 0.1615

> bartlett.test(Eggs[Day=="2DBA"] ~ Trt[Day=="2DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "2DBA"] by Trt[Day == "2DBA"]
```

```
Bartlett's K-squared = 1.8826, df = 2, p-value = 0.3901

> bartlett.test(Eggs[Day=="31DAA"] ~ Trt[Day=="31DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "31DAA"] by Trt[Day == "31DAA"]
Bartlett's K-squared = 2.2262, df = 2, p-value = 0.3285

> bartlett.test(Eggs[Day=="35DAA"] ~ Trt[Day=="35DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "35DAA"] by Trt[Day == "35DAA"]
Bartlett's K-squared = 1.9071, df = 2, p-value = 0.3854

> bartlett.test(Eggs[Day=="3DAA"] ~ Trt[Day=="3DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "3DAA"] by Trt[Day == "3DAA"]
Bartlett's K-squared = 8.4606, df = 2, p-value = 0.01455

> bartlett.test(Eggs[Day=="54DAA"] ~ Trt[Day=="54DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "54DAA"] by Trt[Day == "54DAA"]
Bartlett's K-squared = 0.96934, df = 2, p-value = 0.6159

> bartlett.test(Eggs[Day=="69DAA"] ~ Trt[Day=="69DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "69DAA"] by Trt[Day == "69DAA"]
Bartlett's K-squared = 5.6703, df = 2, p-value = 0.05871

> bartlett.test(Eggs[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 1.0483, df = 2, p-value = 0.5921

> bartlett.test(Eggs[Day=="8DBA"] ~ Trt[Day=="8DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "8DBA"] by Trt[Day == "8DBA"]
Bartlett's K-squared = 2.3978, df = 2, p-value = 0.3015
```

```
> bartlett.test(Eggs[Day=="98DAA"] ~ Trt[Day=="98DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "98DAA"] by Trt[Day == "98DAA"]
Bartlett's K-squared = Inf, df = 2, p-value < 2.2e-16

> bartlett.test(Eggs[Day=="OVRW"] ~ Trt[Day=="OVRW"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Eggs[Day == "OVRW"] by Trt[Day == "OVRW"]
Bartlett's K-squared = 2.972, df = 2, p-value = 0.2263

> bartlett.test(Larvae[Day=="14DAA"] ~ Trt[Day=="14DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "14DAA"] by Trt[Day == "14DAA"]
Bartlett's K-squared = 1.8487, df = 2, p-value = 0.3968

> bartlett.test(Larvae[Day=="20DAA"] ~ Trt[Day=="20DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "20DAA"] by Trt[Day == "20DAA"]
Bartlett's K-squared = 0.4654, df = 2, p-value = 0.7924

> bartlett.test(Larvae[Day=="24DAA"] ~ Trt[Day=="24DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "24DAA"] by Trt[Day == "24DAA"]
Bartlett's K-squared = 0.026643, df = 2, p-value = 0.9868

> bartlett.test(Larvae[Day=="2DBA"] ~ Trt[Day=="2DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "2DBA"] by Trt[Day == "2DBA"]
Bartlett's K-squared = 1.3265, df = 2, p-value = 0.5152

> bartlett.test(Larvae[Day=="31DAA"] ~ Trt[Day=="31DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "31DAA"] by Trt[Day == "31DAA"]
Bartlett's K-squared = 0.45375, df = 2, p-value = 0.797

> bartlett.test(Larvae[Day=="35DAA"] ~ Trt[Day=="35DAA"], Tunnel1)
```

```
        Bartlett test of homogeneity of variances

data:  Larvae[Day == "35DAA"] by Trt[Day == "35DAA"]
Bartlett's K-squared = 35.804, df = 2, p-value = 1.68e-08

> bartlett.test(Larvae[Day=="3DAA"] ~ Trt[Day=="3DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "3DAA"] by Trt[Day == "3DAA"]
Bartlett's K-squared = 0.97562, df = 2, p-value = 0.614

> bartlett.test(Larvae[Day=="54DAA"] ~ Trt[Day=="54DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "54DAA"] by Trt[Day == "54DAA"]
Bartlett's K-squared = 4.1852, df = 2, p-value = 0.1234

> bartlett.test(Larvae[Day=="69DAA"] ~ Trt[Day=="69DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "69DAA"] by Trt[Day == "69DAA"]
Bartlett's K-squared = 0.99816, df = 2, p-value = 0.6071

> bartlett.test(Larvae[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 1.9667, df = 2, p-value = 0.374

> bartlett.test(Larvae[Day=="8DBA"] ~ Trt[Day=="8DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "8DBA"] by Trt[Day == "8DBA"]
Bartlett's K-squared = 2.7952, df = 2, p-value = 0.2472

> bartlett.test(Larvae[Day=="98DAA"] ~ Trt[Day=="98DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Larvae[Day == "98DAA"] by Trt[Day == "98DAA"]
Bartlett's K-squared = 8.4673, df = 2, p-value = 0.0145

> bartlett.test(Larvae[Day=="OVRW"] ~ Trt[Day=="OVRW"], Tunnel1)

        Bartlett test of homogeneity of variances
```

```
data:  Larvae[Day == "OVRW"] by Trt[Day == "OVRW"]
Bartlett's K-squared = 1.7466, df = 2, p-value = 0.4176

> bartlett.test(Pupae[Day=="14DAA"] ~ Trt[Day=="14DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "14DAA"] by Trt[Day == "14DAA"]
Bartlett's K-squared = 1.3476, df = 2, p-value = 0.5098

> bartlett.test(Pupae[Day=="20DAA"] ~ Trt[Day=="20DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "20DAA"] by Trt[Day == "20DAA"]
Bartlett's K-squared = 2.8713, df = 2, p-value = 0.238

> bartlett.test(Pupae[Day=="24DAA"] ~ Trt[Day=="24DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "24DAA"] by Trt[Day == "24DAA"]
Bartlett's K-squared = 2.6292, df = 2, p-value = 0.2686

> bartlett.test(Pupae[Day=="2DBA"] ~ Trt[Day=="2DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "2DBA"] by Trt[Day == "2DBA"]
Bartlett's K-squared = 2.1982, df = 2, p-value = 0.3332

> bartlett.test(Pupae[Day=="31DAA"] ~ Trt[Day=="31DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "31DAA"] by Trt[Day == "31DAA"]
Bartlett's K-squared = 1.1591, df = 2, p-value = 0.5601

> bartlett.test(Pupae[Day=="35DAA"] ~ Trt[Day=="35DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "35DAA"] by Trt[Day == "35DAA"]
Bartlett's K-squared = 4.7142, df = 2, p-value = 0.09469

> bartlett.test(Pupae[Day=="3DAA"] ~ Trt[Day=="3DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "3DAA"] by Trt[Day == "3DAA"]
Bartlett's K-squared = 0.58143, df = 2, p-value = 0.7477
```

```
> bartlett.test(Pupae[Day=="54DAA"] ~ Trt[Day=="54DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "54DAA"] by Trt[Day == "54DAA"]
Bartlett's K-squared = 3.8513, df = 2, p-value = 0.1458

> bartlett.test(Pupae[Day=="69DAA"] ~ Trt[Day=="69DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "69DAA"] by Trt[Day == "69DAA"]
Bartlett's K-squared = 2.4276, df = 2, p-value = 0.2971

> bartlett.test(Pupae[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 0.55386, df = 2, p-value = 0.7581

> bartlett.test(Pupae[Day=="8DBA"] ~ Trt[Day=="8DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "8DBA"] by Trt[Day == "8DBA"]
Bartlett's K-squared = 0.22259, df = 2, p-value = 0.8947

> bartlett.test(Pupae[Day=="98DAA"] ~ Trt[Day=="98DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "98DAA"] by Trt[Day == "98DAA"]
Bartlett's K-squared = 1.8073, df = 2, p-value = 0.4051

> bartlett.test(Pupae[Day=="OVRW"] ~ Trt[Day=="OVRW"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pupae[Day == "OVRW"] by Trt[Day == "OVRW"]
Bartlett's K-squared = 4.4673, df = 2, p-value = 0.1071

> bartlett.test(Brood[Day=="14DAA"] ~ Trt[Day=="14DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "14DAA"] by Trt[Day == "14DAA"]
Bartlett's K-squared = 0.68581, df = 2, p-value = 0.7097

> bartlett.test(Brood[Day=="20DAA"] ~ Trt[Day=="20DAA"], Tunnel1)
```

```
        Bartlett test of homogeneity of variances

data:  Brood[Day == "20DAA"] by Trt[Day == "20DAA"]
Bartlett's K-squared = 3.5484, df = 2, p-value = 0.1696

> bartlett.test(Brood[Day=="24DAA"] ~ Trt[Day=="24DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "24DAA"] by Trt[Day == "24DAA"]
Bartlett's K-squared = 3.3842, df = 2, p-value = 0.1841

> bartlett.test(Brood[Day=="2DBA"] ~ Trt[Day=="2DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "2DBA"] by Trt[Day == "2DBA"]
Bartlett's K-squared = 0.32918, df = 2, p-value = 0.8482

> bartlett.test(Brood[Day=="31DAA"] ~ Trt[Day=="31DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "31DAA"] by Trt[Day == "31DAA"]
Bartlett's K-squared = 1.0664, df = 2, p-value = 0.5867

> bartlett.test(Brood[Day=="35DAA"] ~ Trt[Day=="35DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "35DAA"] by Trt[Day == "35DAA"]
Bartlett's K-squared = 0.97951, df = 2, p-value = 0.6128

> bartlett.test(Brood[Day=="3DAA"] ~ Trt[Day=="3DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "3DAA"] by Trt[Day == "3DAA"]
Bartlett's K-squared = 0.3686, df = 2, p-value = 0.8317

> bartlett.test(Brood[Day=="54DAA"] ~ Trt[Day=="54DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "54DAA"] by Trt[Day == "54DAA"]
Bartlett's K-squared = 4.0064, df = 2, p-value = 0.1349

> bartlett.test(Brood[Day=="69DAA"] ~ Trt[Day=="69DAA"], Tunnel1)

        Bartlett test of homogeneity of variances
```

```
data:  Brood[Day == "69DAA"] by Trt[Day == "69DAA"]
Bartlett's K-squared = 1.4546, df = 2, p-value = 0.4832

> bartlett.test(Brood[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 1.6838, df = 2, p-value = 0.4309

> bartlett.test(Brood[Day=="8DBA"] ~ Trt[Day=="8DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "8DBA"] by Trt[Day == "8DBA"]
Bartlett's K-squared = 2.2213, df = 2, p-value = 0.3293

> bartlett.test(Brood[Day=="98DAA"] ~ Trt[Day=="98DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "98DAA"] by Trt[Day == "98DAA"]
Bartlett's K-squared = 14.154, df = 2, p-value = 0.0008441

> bartlett.test(Brood[Day=="OVRW"] ~ Trt[Day=="OVRW"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Brood[Day == "OVRW"] by Trt[Day == "OVRW"]
Bartlett's K-squared = 5.7601, df = 2, p-value = 0.05613

> bartlett.test(Nectar[Day=="14DAA"] ~ Trt[Day=="14DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "14DAA"] by Trt[Day == "14DAA"]
Bartlett's K-squared = 0.9991, df = 2, p-value = 0.6068

> bartlett.test(Nectar[Day=="20DAA"] ~ Trt[Day=="20DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "20DAA"] by Trt[Day == "20DAA"]
Bartlett's K-squared = 2.7482, df = 2, p-value = 0.2531

> bartlett.test(Nectar[Day=="24DAA"] ~ Trt[Day=="24DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "24DAA"] by Trt[Day == "24DAA"]
```

```
Bartlett's K-squared = 2.9919, df = 2, p-value = 0.224

> bartlett.test(Nectar[Day=="2DBA"] ~ Trt[Day=="2DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "2DBA"] by Trt[Day == "2DBA"]
Bartlett's K-squared = 1.9679, df = 2, p-value = 0.3738

> bartlett.test(Nectar[Day=="31DAA"] ~ Trt[Day=="31DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "31DAA"] by Trt[Day == "31DAA"]
Bartlett's K-squared = 1.7295, df = 2, p-value = 0.4212

> bartlett.test(Nectar[Day=="35DAA"] ~ Trt[Day=="35DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "35DAA"] by Trt[Day == "35DAA"]
Bartlett's K-squared = 0.59158, df = 2, p-value = 0.7439

> bartlett.test(Nectar[Day=="3DAA"] ~ Trt[Day=="3DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "3DAA"] by Trt[Day == "3DAA"]
Bartlett's K-squared = 1.112, df = 2, p-value = 0.5735

> bartlett.test(Nectar[Day=="54DAA"] ~ Trt[Day=="54DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "54DAA"] by Trt[Day == "54DAA"]
Bartlett's K-squared = 5.2054, df = 2, p-value = 0.07407

> bartlett.test(Nectar[Day=="69DAA"] ~ Trt[Day=="69DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "69DAA"] by Trt[Day == "69DAA"]
Bartlett's K-squared = 3.0175, df = 2, p-value = 0.2212

> bartlett.test(Nectar[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 0.81121, df = 2, p-value = 0.6666
```

```
> bartlett.test(Nectar[Day=="8DBA"] ~ Trt[Day=="8DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "8DBA"] by Trt[Day == "8DBA"]
Bartlett's K-squared = 2.6695, df = 2, p-value = 0.2632

> bartlett.test(Nectar[Day=="98DAA"] ~ Trt[Day=="98DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "98DAA"] by Trt[Day == "98DAA"]
Bartlett's K-squared = 7.3243, df = 2, p-value = 0.02568

> bartlett.test(Nectar[Day=="OVRW"] ~ Trt[Day=="OVRW"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Nectar[Day == "OVRW"] by Trt[Day == "OVRW"]
Bartlett's K-squared = 2.0489, df = 2, p-value = 0.359

> bartlett.test(Pollen[Day=="14DAA"] ~ Trt[Day=="14DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "14DAA"] by Trt[Day == "14DAA"]
Bartlett's K-squared = 5.3996, df = 2, p-value = 0.06722

> bartlett.test(Pollen[Day=="20DAA"] ~ Trt[Day=="20DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "20DAA"] by Trt[Day == "20DAA"]
Bartlett's K-squared = 1.501, df = 2, p-value = 0.4721

> bartlett.test(Pollen[Day=="24DAA"] ~ Trt[Day=="24DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "24DAA"] by Trt[Day == "24DAA"]
Bartlett's K-squared = 0.52227, df = 2, p-value = 0.7702

> bartlett.test(Pollen[Day=="2DBA"] ~ Trt[Day=="2DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "2DBA"] by Trt[Day == "2DBA"]
Bartlett's K-squared = 0.003201, df = 2, p-value = 0.9984

> bartlett.test(Pollen[Day=="31DAA"] ~ Trt[Day=="31DAA"], Tunnel1)
```

```
        Bartlett test of homogeneity of variances

data:  Pollen[Day == "31DAA"] by Trt[Day == "31DAA"]
Bartlett's K-squared = 1.1973, df = 2, p-value = 0.5495

> bartlett.test(Pollen[Day=="35DAA"] ~ Trt[Day=="35DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "35DAA"] by Trt[Day == "35DAA"]
Bartlett's K-squared = 1.6283, df = 2, p-value = 0.443

> bartlett.test(Pollen[Day=="3DAA"] ~ Trt[Day=="3DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "3DAA"] by Trt[Day == "3DAA"]
Bartlett's K-squared = 1.77, df = 2, p-value = 0.4127

> bartlett.test(Pollen[Day=="54DAA"] ~ Trt[Day=="54DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "54DAA"] by Trt[Day == "54DAA"]
Bartlett's K-squared = 0.0077718, df = 2, p-value = 0.9961

> bartlett.test(Pollen[Day=="69DAA"] ~ Trt[Day=="69DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "69DAA"] by Trt[Day == "69DAA"]
Bartlett's K-squared = 0.71659, df = 2, p-value = 0.6989

> bartlett.test(Pollen[Day=="8DAA"] ~ Trt[Day=="8DAA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "8DAA"] by Trt[Day == "8DAA"]
Bartlett's K-squared = 1.6261, df = 2, p-value = 0.4435

> bartlett.test(Pollen[Day=="8DBA"] ~ Trt[Day=="8DBA"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "8DBA"] by Trt[Day == "8DBA"]
Bartlett's K-squared = 2.4096, df = 2, p-value = 0.2998

> bartlett.test(Pollen[Day=="98DAA"] ~ Trt[Day=="98DAA"], Tunnel1)

        Bartlett test of homogeneity of variances
```

```
data:  Pollen[Day == "98DAA"] by Trt[Day == "98DAA"]
Bartlett's K-squared = 0.74865, df = 2, p-value = 0.6878

> bartlett.test(Pollen[Day=="OVRW"] ~ Trt[Day=="OVRW"], Tunnel1)

        Bartlett test of homogeneity of variances

data:  Pollen[Day == "OVRW"] by Trt[Day == "OVRW"]
Bartlett's K-squared = 1.0084, df = 2, p-value = 0.604

> DunnettTest(Adults~Trt, data=Tunnel1[Tunnel1$Day=='20DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -292.5000 -3414.349 2829.349 0.9626
T2-Cont -346.6667 -3468.516 2775.183 0.9480

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Adults~Trt, data=Tunnel1[Tunnel1$Day=='2DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -108.3333 -1747.277 1530.611 0.9811
T2-Cont -617.5000 -2256.444 1021.444 0.5686

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Adults~Trt, data=Tunnel1[Tunnel1$Day=='35DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
          diff    lwr.ci   upr.ci   pval
T1-Cont -390.0 -2753.161 1973.161 0.8899
T2-Cont  292.5 -2070.661 2655.661 0.9359

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Adults~Trt, data=Tunnel1[Tunnel1$Day=='54DAA',])
```

```
  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -487.5000 -2326.332 1351.332 0.7467
T2-Cont  530.8333 -1307.999 2369.666 0.7094

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Adults~Trt, data=Tunnel1[Tunnel1$Day=='24DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff    lwr.ci   upr.ci   pval
T1-Cont   65 -2477.736 2607.736 0.9971
T2-Cont  455 -2087.736 2997.736 0.8723

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Adults~Trt, data=Tunnel1[Tunnel1$Day=='8DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
T1-Cont -1570.833 -4125.883  984.2164 0.2593
T2-Cont -1213.333 -3768.383 1341.7164 0.4236

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Adults~Trt, data=Tunnel1[Tunnel1$Day=='69DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
T1-Cont -660.8333 -2313.585  991.9182 0.5328
T2-Cont  433.3333 -1219.418 2086.0849 0.7513

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Adults~Trt, data=Tunnel1[Tunnel1$Day=='98DAA',])
```

```
  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff     lwr.ci   upr.ci   pval
T1-Cont  86.66667 -1475.5851 1648.918 0.9867
T2-Cont 964.16667  -598.0851 2526.418 0.2570

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Adults~Trt, data=Tunnel1[Tunnel1$Day=='OVRW',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -758.3333 -3169.889 1653.223 0.6680
T2-Cont  119.1667 -2292.389 2530.723 0.9894

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
> DunnettTest(Eggs~Trt, data=Tunnel1[Tunnel1$Day=='2ODAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff     lwr.ci    upr.ci   pval
T1-Cont  666.6667  -386.9641 1720.2974 0.2422
T2-Cont -533.3333 -1586.9641  520.2974 0.3821

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Eggs~Trt, data=Tunnel1[Tunnel1$Day=='2DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff    lwr.ci   upr.ci   pval
T1-Cont  700 -1909.906 3309.906 0.7419
T2-Cont  300 -2309.906 2909.906 0.9444

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> DunnettTest(Eggs~Trt, data=Tunnel1[Tunnel1$Day=='35DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
T1-Cont -900.0000 -2762.485  962.4849 0.4123
T2-Cont -533.3333 -2395.818 1329.1515 0.7131

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Eggs~Trt, data=Tunnel1[Tunnel1$Day=='54DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff   lwr.ci    upr.ci   pval
T1-Cont  66.66667 -736.732  870.0654 0.9705
T2-Cont 266.66667 -536.732 1070.0654 0.6400

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Eggs~Trt, data=Tunnel1[Tunnel1$Day=='8DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
            diff    lwr.ci   upr.ci   pval
T1-Cont 866.6667 -300.1409 2033.474 0.1561
T2-Cont 600.0000 -566.8075 1766.808 0.3719

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Eggs~Trt, data=Tunnel1[Tunnel1$Day=='8DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont  166.6667 -1961.621 2294.954 0.9737
T2-Cont -833.3333 -2961.621 1294.954 0.5456

---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Eggs~Trt, data=Tunnel1[Tunnel1$Day=='14DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
            diff    lwr.ci   upr.ci   pval
T1-Cont 400.0000 -1822.726 2622.726 0.8709
T2-Cont 133.3333 -2089.392 2356.059 0.9844

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Eggs~Trt, data=Tunnel1[Tunnel1$Day=='69DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont 200.00000 -471.2527 871.2527 0.6946
T2-Cont  66.66667 -604.5860 737.9193 0.9581

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
> DunnettTest(Larvae~Trt, data=Tunnel1[Tunnel1$Day=='20DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff    lwr.ci   upr.ci   pval
T1-Cont -400 -4052.782 3252.782 0.9494
T2-Cont 2200 -1452.782 5852.782 0.2717

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Larvae~Trt, data=Tunnel1[Tunnel1$Day=='2DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -566.6667 -4133.589 3000.256 0.8974
T2-Cont -200.0000 -3766.923 3366.923 0.9864
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Larvae~Trt, data=Tunnel1[Tunnel1$Day=='31DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -730.0000 -3101.778 1641.778 0.6788
T2-Cont  266.6667 -2105.111 2638.444 0.9467

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Larvae~Trt, data=Tunnel1[Tunnel1$Day=='24DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -933.3333 -4001.075 2134.409 0.6845
T2-Cont -433.3333 -3501.075 2634.409 0.9176

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Larvae~Trt, data=Tunnel1[Tunnel1$Day=='8DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
            diff     lwr.ci   upr.ci   pval
T1-Cont 200.0000 -1433.7357 1833.736 0.9373
T2-Cont 733.3333  -900.4023 2367.069 0.4600

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Larvae~Trt, data=Tunnel1[Tunnel1$Day=='8DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -286.6667 -4466.167 3892.834 0.9797
```

```
T2-Cont  546.6667 -3632.834 4726.167 0.9288

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Larvae~Trt, data=Tunnel1[Tunnel1$Day=='69DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
            diff     lwr.ci    upr.ci   pval
T1-Cont 266.6667 -348.37456  881.7079 0.4822
T2-Cont 700.0000   84.95878 1315.0412 0.0259 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Larvae~Trt, data=Tunnel1[Tunnel1$Day=='OVRW',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff     lwr.ci    upr.ci   pval
T1-Cont -200.0000 -1324.8679  924.8679 0.8737
T2-Cont  266.6667  -858.2012 1391.5346 0.7900

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='2ODAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci   upr.ci   pval
T1-Cont -1066.6667 -4831.897 2698.564 0.7180
T2-Cont   566.6667 -3198.564 4331.897 0.9072

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='2DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
```

```
             diff    lwr.ci   upr.ci   pval
T1-Cont  366.6667 -3994.783 4728.116 0.9697
T2-Cont 1366.6667 -2994.783 5728.116 0.6698

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='31DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
               diff    lwr.ci   upr.ci   pval
T1-Cont -1400.00000 -4677.710 1877.710 0.4917
T2-Cont   -66.66667 -3344.377 3211.043 0.9982

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='35DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -1700.0000 -5016.887 1616.887 0.3740
T2-Cont  -166.6667 -3483.554 3150.220 0.9890

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='3DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -1466.6667 -4081.972 1148.639 0.3161
T2-Cont  -166.6667 -2781.972 2448.639 0.9824

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='54DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level
```

```
$Cont
             diff   lwr.ci    upr.ci   pval
T1-Cont -2033.333 -4189.61  122.9432 0.0650 .
T2-Cont -1133.333 -3289.61 1022.9432 0.3577

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='8DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont  433.3333 -3462.192 4328.858 0.9478
T2-Cont -500.0000 -4395.525 3395.525 0.9313

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='8DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
            diff    lwr.ci   upr.ci   pval
T1-Cont 1433.333 -3277.243 6143.910 0.6844
T2-Cont 1566.667 -3143.910 6277.243 0.6389

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='14DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -700.0000 -6025.254 4625.254 0.9281
T2-Cont -433.3333 -5758.588 4891.921 0.9716

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='69DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level
```

```
$Cont
        diff    lwr.ci   upr.ci   pval
T1-Cont -600 -3880.802 2680.802 0.8671
T2-Cont -600 -3880.802 2680.802 0.8671

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='98DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff     lwr.ci    upr.ci   pval
T1-Cont -433.3333 -1459.4051  592.7384 0.4988
T2-Cont  100.0000  -926.0718 1126.0718 0.9596

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pupae~Trt, data=Tunnel1[Tunnel1$Day=='OVRW',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -433.3333 -4095.879 3229.212 0.9412
T2-Cont  766.6667 -2895.879 4429.212 0.8307

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='2ODAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
            diff    lwr.ci   upr.ci   pval
T1-Cont -800.000 -5628.525 4028.525 0.8891
T2-Cont 2233.333 -2595.192 7061.859 0.4407

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='2DBA',])
```

```
  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont  566.6667 -6878.892 8012.226 0.9751
T2-Cont 1500.0000 -5945.559 8945.559 0.8418

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='31DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci   upr.ci   pval
T1-Cont -2966.6667 -8138.025 2204.692 0.3018
T2-Cont  -466.6667 -5638.025 4704.692 0.9652

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='35DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
         diff    lwr.ci   upr.ci   pval
T1-Cont -3800 -9092.534 1492.534 0.1729
T2-Cont  1000 -4292.534 6292.534 0.8590

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='3DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci   upr.ci   pval
T1-Cont -1466.6667 -5875.271 2941.937 0.6387
T2-Cont   766.6667 -3641.937 5175.271 0.8788

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='54DAA',])
```

```
  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
T1-Cont -1833.333 -4303.870  637.2037 0.1566
T2-Cont -1100.000 -3570.537 1370.5371 0.4652

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='24DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -1533.333 -7401.505 4334.838 0.7527
T2-Cont  1166.667 -4701.505 7034.838 0.8455

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='8DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont 1500.0000 -3812.987 6812.987 0.7195
T2-Cont  833.3333 -4479.654 6146.320 0.8998

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='8DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont   0.00000 -6353.715 6353.715 1.0000
T2-Cont -66.66667 -6420.381 6287.048 0.9995

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='14DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -166.6667 -7877.686 7544.353 0.9980
T2-Cont 1200.0000 -6511.020 8911.020 0.9013

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='69DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -133.3333 -3704.703 3438.036 0.9939
T2-Cont  166.6667 -3404.703 3738.036 0.9905

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Brood~Trt, data=Tunnel1[Tunnel1$Day=='OVRW',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci   upr.ci   pval
T1-Cont   66.66667 -4275.636 4408.969 0.9990
T2-Cont 1666.66667 -2675.636 6008.969 0.5576

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='20DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci   upr.ci   pval
T1-Cont -1033.3333 -5654.331 3587.664 0.8100
T2-Cont   433.3333 -4187.664 5054.331 0.9625

---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='2DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff  lwr.ci   upr.ci   pval
T1-Cont -433.3333 -4171.3 3304.633 0.9435
T2-Cont 1066.6667 -2671.3 4804.633 0.7147

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='31DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -1033.333 -5744.003 3677.337 0.8163
T2-Cont  1200.000 -3510.670 5910.670 0.7629

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='35DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff    lwr.ci   upr.ci   pval
T1-Cont -500 -4337.486 3337.486 0.9293
T2-Cont 1100 -2737.486 4937.486 0.7126

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='3DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -666.6667 -4363.598 3030.265 0.8704
T2-Cont  533.3333 -3163.598 4230.265 0.9143
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='54DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff     lwr.ci   upr.ci   pval
T1-Cont -2566.6667 -11201.071 6067.738 0.6957
T2-Cont  -566.6667  -9201.071 8067.738 0.9814

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='24DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -766.6667 -4861.598 3328.264 0.8613
T2-Cont 1333.3333 -2761.598 5428.264 0.6501

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='8DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff     lwr.ci   upr.ci   pval
T1-Cont -100 -3780.9167 3580.917 0.9968
T2-Cont 3100  -580.9167 6780.917 0.1021

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='8DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci   upr.ci   pval
T1-Cont   66.66667 -4832.741 4966.074 0.9992
T2-Cont -666.66667 -5566.074 4232.741 0.9233
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='14DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -266.6667 -4434.696 3901.362 0.9823
T2-Cont 2766.6667 -1401.362 6934.696 0.2148

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Nectar~Trt, data=Tunnel1[Tunnel1$Day=='69DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
            diff    lwr.ci   upr.ci   pval
T1-Cont -100.000 -9168.100  8968.10 0.9995
T2-Cont 4066.667 -5001.433 13134.77 0.4606

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
> DunnettTest(Pollen~Trt, data=Tunnel1[Tunnel1$Day=='20DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -1366.667 -3737.952 1004.619 0.2989
T2-Cont  -500.000 -2871.285 1871.285 0.8286

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pollen~Trt, data=Tunnel1[Tunnel1$Day=='2DBA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff     lwr.ci   upr.ci   pval
```

```
T1-Cont  300 -1067.5585 1667.558 0.8163
T2-Cont  500  -867.5585 1867.558 0.5862

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pollen~Trt, data=Tunnel1[Tunnel1$Day=='31DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
T1-Cont -1100.0000 -3119.442  919.4423 0.3347
T2-Cont  -833.3333 -2852.776 1186.1090 0.5133

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pollen~Trt, data=Tunnel1[Tunnel1$Day=='35DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
T1-Cont -1000.0000 -2643.958  643.9584 0.2657
T2-Cont  -433.3333 -2077.292 1210.6250 0.7491

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pollen~Trt, data=Tunnel1[Tunnel1$Day=='3DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont  -66.66667 -2088.509 1955.176 0.9953
T2-Cont -333.33333 -2355.176 1688.509 0.8901

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pollen~Trt, data=Tunnel1[Tunnel1$Day=='54DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
```

```
             diff     lwr.ci    upr.ci   pval
T1-Cont -166.6667 -1059.9719  726.6385 0.8622
T2-Cont  400.0000  -493.3052 1293.3052 0.4616

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pollen~Trt, data=Tunnel1[Tunnel1$Day=='24DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -1966.667 -4148.149 214.8161 0.0785 .
T2-Cont -1400.000 -3581.483 781.4828 0.2340

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pollen~Trt, data=Tunnel1[Tunnel1$Day=='8DAA',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -400.0000 -1771.422 971.4217 0.7046
T2-Cont -433.3333 -1804.755 938.0883 0.6656

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Pollen~Trt, data=Tunnel1[Tunnel1$Day=='OVRW',]
+ )

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont  100.0000 -664.0197 864.0197 0.9287
T2-Cont -166.6667 -930.6864 597.3531 0.8180

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Tunnel1[Tunnel1$Day=="14DAA",], pairwise.wilcox.test(Adults, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test
```

```
data:  Adults and Trt

   Cont T1
T1 0.45 -
T2 1.00 0.93

P value adjustment method: bonferroni
Warning message:
In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="31DAA",], pairwise.wilcox.test(Adults, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Adults and Trt

   Cont  T1
T1 1.000 -
T2 0.089 0.889

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="8DBA",], pairwise.wilcox.test(Adults, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Adults and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning message:
In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="24DAA",], pairwise.wilcox.test(Eggs, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Eggs and Trt
```

```
   Cont  T1
T1 0.188 -
T2 1.000 0.098

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="31DAA",], pairwise.wilcox.test(Eggs, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Eggs and Trt

   Cont T1
T1 0.68 -
T2 1.00 1.00

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="3DAA",], pairwise.wilcox.test(Eggs, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Eggs and Trt

   Cont T1
T1 1.00 -
T2 0.31 0.78

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
```

```
> with(Tunnel1[Tunnel1$Day=="98DAA",], pairwise.wilcox.test(Eggs, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Eggs and Trt

   Cont T1
T1 0.35 -
T2 0.35 -

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="OVRW",], pairwise.wilcox.test(Eggs, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Eggs and Trt

   Cont  T1
T1 0.017 -
T2 0.097 1.000

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="14DAA",], pairwise.wilcox.test(Larvae, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Larvae and Trt

   Cont T1
T1 1.00 -
T2 0.77 0.78

P value adjustment method: bonferroni
Warning messages:
```

```
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="35DAA",], pairwise.wilcox.test(Larvae, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Larvae and Trt

   Cont T1
T1 1.00 -
T2 0.11 0.23

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="3DAA",], pairwise.wilcox.test(Larvae, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Larvae and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="98DAA",], pairwise.wilcox.test(Larvae, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Larvae and Trt
```

```
   Cont T1
T1 0.64 -
T2 1.00 0.64

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="54DAA",], pairwise.wilcox.test(Larvae, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Larvae and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="24DAA",], pairwise.wilcox.test(Pupae, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Pupae and Trt

   Cont T1
T1 0.93 -
T2 0.89 0.12

P value adjustment method: bonferroni
Warning message:
In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="98DAA",], pairwise.wilcox.test(Brood, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test
```

```
data:  Brood and Trt

   Cont T1
T1 0.31 -
T2 1.00 0.99

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="OVRW",], pairwise.wilcox.test(Nectar, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Nectar and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="98DAA",], pairwise.wilcox.test(Nectar, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Nectar and Trt

   Cont T1
T1 1.00 -
T2 1.00 0.68

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
```

```
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="14DAA",], pairwise.wilcox.test(Pollen, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Pollen and Trt

   Cont T1
T1 1.00 -
T2 0.87 1.00

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="69DAA",], pairwise.wilcox.test(Pollen, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Pollen and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="8DBA",], pairwise.wilcox.test(Pollen, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Pollen and Trt

   Cont T1
T1 1.00 -
T2 0.27 0.13

P value adjustment method: bonferroni
```

```
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Tunnel1[Tunnel1$Day=="98DAA",], pairwise.wilcox.test(Pollen, Trt, p.ad
j = 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Pollen and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties

> with(Mort1, tapply(Mortality, Day, shapiro.test))
$`0`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.87256, p-value = 0.01961


$`1`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.95228, p-value = 0.462


$`2`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96771, p-value = 0.7537
```

```
$`3`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.98174, p-value = 0.9661


$`4`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97661, p-value = 0.9085


$`5`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.91819, p-value = 0.1201


$`6`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93088, p-value = 0.2012


$`7`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.957, p-value = 0.5449


$`8`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.81817, p-value = 0.002775


$`9`
```

```
        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.92944, p-value = 0.1899


$`10`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.95021, p-value = 0.4283


$`11`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.86445, p-value = 0.01443


$`12`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.92785, p-value = 0.178


$`13`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.758, p-value = 0.0004108


$`14`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.89998, p-value = 0.05741


$`15`

        Shapiro-Wilk normality test

data:  X[[i]]
```

```
W = 0.82437, p-value = 0.003427


$`16`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96318, p-value = 0.664


$`17`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.92976, p-value = 0.1923


$`18`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.95987, p-value = 0.5991


$`19`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.76776, p-value = 0.0005511


$`20`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.90043, p-value = 0.05845


$`21`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.95443, p-value = 0.4986
```

```
$`22`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93789, p-value = 0.2666


$`23`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.9354, p-value = 0.2414


$`24`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.88312, p-value = 0.02946


$`25`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.85696, p-value = 0.01093


$`26`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.86795, p-value = 0.01647


$`27`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93928, p-value = 0.2817


$`28`

        Shapiro-Wilk normality test
```

```
data:  X[[i]]
W = 0.94446, p-value = 0.3449


$`29`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96846, p-value = 0.7683


$`30`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.89073, p-value = 0.03972


$`31`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.927, p-value = 0.1719


$`32`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97029, p-value = 0.8031


$`33`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93712, p-value = 0.2585


$`34`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93635, p-value = 0.2507
```

```
$`35`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96751, p-value = 0.7497


$`36`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.9232, p-value = 0.1473


$`37`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.84938, p-value = 0.008279


$`38`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.84071, p-value = 0.006064


$`39`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.76266, p-value = 0.0004723


$`40`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.68328, p-value = 5.137e-05

> bartlett.test(Mortality[Day=="0"] ~ Trt[Day=="0"], Mort1)
```

```
        Bartlett test of homogeneity of variances

data:  Mortality[Day == "0"] by Trt[Day == "0"]
Bartlett's K-squared = 17.829, df = 2, p-value = 0.0001344

> bartlett.test(Mortality[Day=="1"] ~ Trt[Day=="1"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "1"] by Trt[Day == "1"]
Bartlett's K-squared = 0.23569, df = 2, p-value = 0.8888

> bartlett.test(Mortality[Day=="2"] ~ Trt[Day=="2"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "2"] by Trt[Day == "2"]
Bartlett's K-squared = 0.051872, df = 2, p-value = 0.9744

> bartlett.test(Mortality[Day=="3"] ~ Trt[Day=="3"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "3"] by Trt[Day == "3"]
Bartlett's K-squared = 0.61471, df = 2, p-value = 0.7354

> bartlett.test(Mortality[Day=="4"] ~ Trt[Day=="4"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "4"] by Trt[Day == "4"]
Bartlett's K-squared = 1.8774, df = 2, p-value = 0.3911

> bartlett.test(Mortality[Day=="5"] ~ Trt[Day=="5"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "5"] by Trt[Day == "5"]
Bartlett's K-squared = 3.1153, df = 2, p-value = 0.2106

> bartlett.test(Mortality[Day=="6"] ~ Trt[Day=="6"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "6"] by Trt[Day == "6"]
Bartlett's K-squared = 1.0767, df = 2, p-value = 0.5837

> bartlett.test(Mortality[Day=="7"] ~ Trt[Day=="7"], Mort1)

        Bartlett test of homogeneity of variances
```

```
data:  Mortality[Day == "7"] by Trt[Day == "7"]
Bartlett's K-squared = 3.0351, df = 2, p-value = 0.2193

> bartlett.test(Mortality[Day=="8"] ~ Trt[Day=="8"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "8"] by Trt[Day == "8"]
Bartlett's K-squared = 4.7807, df = 2, p-value = 0.0916

> bartlett.test(Mortality[Day=="9"] ~ Trt[Day=="9"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "9"] by Trt[Day == "9"]
Bartlett's K-squared = 3.0952, df = 2, p-value = 0.2128

> bartlett.test(Mortality[Day=="10"] ~ Trt[Day=="10"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "10"] by Trt[Day == "10"]
Bartlett's K-squared = 0.57984, df = 2, p-value = 0.7483

> bartlett.test(Mortality[Day=="11"] ~ Trt[Day=="11"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "11"] by Trt[Day == "11"]
Bartlett's K-squared = 1.7596, df = 2, p-value = 0.4149

> bartlett.test(Mortality[Day=="12"] ~ Trt[Day=="12"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "12"] by Trt[Day == "12"]
Bartlett's K-squared = 1.1082, df = 2, p-value = 0.5746

> bartlett.test(Mortality[Day=="13"] ~ Trt[Day=="13"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "13"] by Trt[Day == "13"]
Bartlett's K-squared = 6.0388, df = 2, p-value = 0.04883

> bartlett.test(Mortality[Day=="14"] ~ Trt[Day=="14"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "14"] by Trt[Day == "14"]
Bartlett's K-squared = 4.276, df = 2, p-value = 0.1179
```

```
> bartlett.test(Mortality[Day=="15"] ~ Trt[Day=="15"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "15"] by Trt[Day == "15"]
Bartlett's K-squared = 4.2116, df = 2, p-value = 0.1217

> bartlett.test(Mortality[Day=="16"] ~ Trt[Day=="16"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "16"] by Trt[Day == "16"]
Bartlett's K-squared = 0.45489, df = 2, p-value = 0.7966

> bartlett.test(Mortality[Day=="17"] ~ Trt[Day=="17"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "17"] by Trt[Day == "17"]
Bartlett's K-squared = 2.8551, df = 2, p-value = 0.2399

> bartlett.test(Mortality[Day=="18"] ~ Trt[Day=="18"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "18"] by Trt[Day == "18"]
Bartlett's K-squared = 3.0215, df = 2, p-value = 0.2207

> bartlett.test(Mortality[Day=="19"] ~ Trt[Day=="19"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "19"] by Trt[Day == "19"]
Bartlett's K-squared = 4.3527, df = 2, p-value = 0.1135

> bartlett.test(Mortality[Day=="20"] ~ Trt[Day=="20"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "20"] by Trt[Day == "20"]
Bartlett's K-squared = 3.4014, df = 2, p-value = 0.1826

> bartlett.test(Mortality[Day=="21"] ~ Trt[Day=="21"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "21"] by Trt[Day == "21"]
Bartlett's K-squared = 6.7648, df = 2, p-value = 0.03397

> bartlett.test(Mortality[Day=="22"] ~ Trt[Day=="22"], Mort1)
```

```
        Bartlett test of homogeneity of variances

data:  Mortality[Day == "22"] by Trt[Day == "22"]
Bartlett's K-squared = 3.824, df = 2, p-value = 0.1478

> bartlett.test(Mortality[Day=="23"] ~ Trt[Day=="23"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "23"] by Trt[Day == "23"]
Bartlett's K-squared = 0.49646, df = 2, p-value = 0.7802

> bartlett.test(Mortality[Day=="24"] ~ Trt[Day=="24"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "24"] by Trt[Day == "24"]
Bartlett's K-squared = 4.4165, df = 2, p-value = 0.1099

> bartlett.test(Mortality[Day=="25"] ~ Trt[Day=="25"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "25"] by Trt[Day == "25"]
Bartlett's K-squared = 4.349, df = 2, p-value = 0.1137

> bartlett.test(Mortality[Day=="26"] ~ Trt[Day=="26"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "26"] by Trt[Day == "26"]
Bartlett's K-squared = 1.0644, df = 2, p-value = 0.5873

> bartlett.test(Mortality[Day=="27"] ~ Trt[Day=="27"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "27"] by Trt[Day == "27"]
Bartlett's K-squared = 4.5569, df = 2, p-value = 0.1024

> bartlett.test(Mortality[Day=="28"] ~ Trt[Day=="28"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "28"] by Trt[Day == "28"]
Bartlett's K-squared = 1.1168, df = 2, p-value = 0.5721

> bartlett.test(Mortality[Day=="29"] ~ Trt[Day=="29"], Mort1)

        Bartlett test of homogeneity of variances
```

```
data:  Mortality[Day == "29"] by Trt[Day == "29"]
Bartlett's K-squared = 1.8836, df = 2, p-value = 0.3899

> bartlett.test(Mortality[Day=="30"] ~ Trt[Day=="30"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "30"] by Trt[Day == "30"]
Bartlett's K-squared = 5.7889, df = 2, p-value = 0.05533

> bartlett.test(Mortality[Day=="31"] ~ Trt[Day=="31"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "31"] by Trt[Day == "31"]
Bartlett's K-squared = 1.5321, df = 2, p-value = 0.4648

> bartlett.test(Mortality[Day=="32"] ~ Trt[Day=="32"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "32"] by Trt[Day == "32"]
Bartlett's K-squared = 6.3762, df = 2, p-value = 0.04125

> bartlett.test(Mortality[Day=="33"] ~ Trt[Day=="33"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "33"] by Trt[Day == "33"]
Bartlett's K-squared = 3.9077, df = 2, p-value = 0.1417

> bartlett.test(Mortality[Day=="34"] ~ Trt[Day=="34"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "34"] by Trt[Day == "34"]
Bartlett's K-squared = 3.6584, df = 2, p-value = 0.1605

> bartlett.test(Mortality[Day=="35"] ~ Trt[Day=="35"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "35"] by Trt[Day == "35"]
Bartlett's K-squared = 0.29109, df = 2, p-value = 0.8646

> bartlett.test(Mortality[Day=="36"] ~ Trt[Day=="36"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "36"] by Trt[Day == "36"]
```

```
Bartlett's K-squared = 2.28, df = 2, p-value = 0.3198

> bartlett.test(Mortality[Day=="37"] ~ Trt[Day=="37"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "37"] by Trt[Day == "37"]
Bartlett's K-squared = 5.7868, df = 2, p-value = 0.05539

> bartlett.test(Mortality[Day=="38"] ~ Trt[Day=="38"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "38"] by Trt[Day == "38"]
Bartlett's K-squared = 5.9762, df = 2, p-value = 0.05038

> bartlett.test(Mortality[Day=="39"] ~ Trt[Day=="39"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "39"] by Trt[Day == "39"]
Bartlett's K-squared = 6.91, df = 2, p-value = 0.03159

> bartlett.test(Mortality[Day=="40"] ~ Trt[Day=="40"], Mort1)

        Bartlett test of homogeneity of variances

data:  Mortality[Day == "40"] by Trt[Day == "40"]
Bartlett's K-squared = 9.7026, df = 2, p-value = 0.007818

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='1',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff     lwr.ci    upr.ci   pval
T1-Cont -3.166667 -14.338656  8.005323 0.7177
T2-Cont  5.333333  -5.838656 16.505323 0.4202

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='2',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
T1-Cont -15.83333 -30.61882 -1.047843 0.0358 *
```

```
T2-Cont -17.50000 -32.28549 -2.714509 0.0208 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='3',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci    pval
T1-Cont -38.33333 -60.64868 -16.01798  0.0015 **
T2-Cont -51.83333 -74.14868 -29.51798 8.6e-05 ***

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='4',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
T1-Cont -10.16667 -29.89338 9.5600516 0.3704
T2-Cont -19.00000 -38.72672 0.7267183 0.0593 .

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='5',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
         diff    lwr.ci    upr.ci   pval
T1-Cont -38.0 -80.33337   4.33337 0.0798 .
T2-Cont -53.5 -95.83337 -11.16663 0.0141 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='6',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
```

```
T1-Cont -35.83333 -73.67748  2.010810 0.0639 .
T2-Cont -44.66667 -82.51081 -6.822524 0.0212 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='8',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff     lwr.ci    upr.ci   pval
T1-Cont   -1 -11.702375  9.702375 0.9628
T2-Cont    1  -9.702375 11.702375 0.9628

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='9',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -6.500000 -24.51968 11.51968 0.5939
T2-Cont -5.666667 -23.68634 12.35301 0.6680

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='12',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
            diff    lwr.ci   upr.ci   pval
T1-Cont 3.166667 -7.194533 13.52787 0.6822
T2-Cont 6.833333 -3.527867 17.19453 0.2184

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='14',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
```

```
             diff     lwr.ci    upr.ci   pval
T1-Cont -2.833333 -11.754038  6.087372 0.6630
T2-Cont  6.333333  -2.587372 15.254038 0.1786

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='15',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
         diff    lwr.ci   upr.ci   pval
T1-Cont  24.0 -18.53286 66.53286 0.3122
T2-Cont -14.5 -57.03286 28.03286 0.6255

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='16',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff     lwr.ci   upr.ci   pval
T1-Cont 10.333333  0.4390129 20.22765 0.0406 *
T2-Cont  1.166667 -8.7276537 11.06099 0.9416

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='17',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff     lwr.ci   upr.ci   pval
T1-Cont  3.5  -9.011384 16.01138 0.7236
T2-Cont  0.5 -12.011384 13.01138 0.9930

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='18',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level
```

```
$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -2.333333 -8.240593 3.573926 0.5403
T2-Cont -2.333333 -8.240593 3.573926 0.5403

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='20',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont -2.833333 -12.29022 6.623551 0.6919
T2-Cont -2.833333 -12.29022 6.623551 0.6919

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='22',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff   lwr.ci   upr.ci   pval
T1-Cont  1.0 -9.45861 11.45861 0.9611
T2-Cont  3.5 -6.95861 13.95861 0.6356

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='23',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci    upr.ci   pval
T1-Cont  1.8333333 -6.801071 10.467738 0.8265
T2-Cont -0.3333333 -8.967738  8.301071 0.9935

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='27',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level
```

```
$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont 0.5000000 -6.962120 7.962120 0.9806
T2-Cont 0.1666667 -7.295454 7.628787 0.9978

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='28',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci   pval
T1-Cont 0.1666667 -8.015494  8.348827 0.9982
T2-Cont 3.3333333 -4.848827 11.515494 0.5213

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='29',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
        diff    lwr.ci   upr.ci   pval
T1-Cont  3.5 -1.979414 8.979414 0.2367
T2-Cont -2.0 -7.479414 3.479414 0.5871

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='31',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci     upr.ci   pval
T1-Cont -2.500000 -6.879305  1.8793052 0.3049
T2-Cont -4.833333 -9.212638 -0.4540282 0.0306 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='33',])

  Dunnett's test for comparing several treatments with a control :
```

```
    95% family-wise confidence level

$Cont
               diff    lwr.ci    upr.ci   pval
T1-Cont   0.8333333 -18.38911 20.055773 0.9918
T2-Cont -17.3333333 -36.55577  1.889106 0.0784 .

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='34',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci   upr.ci   pval
T1-Cont  1.666667 -16.72653 20.05987 0.9649
T2-Cont -8.333333 -26.72653 10.05987 0.4540

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='35',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci   upr.ci   pval
T1-Cont -0.6666667  -9.00891 7.675577 0.9726
T2-Cont -5.8333333 -14.17558 2.508910 0.1865

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(Mortality~Trt, data=Mort1[Mort1$Day=='36',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci     upr.ci   pval
T1-Cont  -1.50000 -14.82782 11.8278229 0.9466
T2-Cont -12.33333 -25.66116  0.9944896 0.0704 .

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Mort1[Mort1$Day=="37",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))
```

```
        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont  T1
T1 0.891 -
T2 0.135 0.047

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="38",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont  T1
T1 0.383 -
T2 0.684 0.073

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="39",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 1.00 -
T2 1.00 0.33

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
```

```
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="40",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 0.72 -
T2 1.00 0.54

P value adjustment method: bonferroni
> with(Mort1[Mort1$Day=="30",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 1.00 -
T2 0.23 0.66

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="32",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 1.00 -
T2 0.69 1.00

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
```

```
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="13",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="21",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning message:
In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="19",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
```

```
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="24",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="25",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont  T1
T1 1.000 -
T2 0.679 0.073

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="26",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
```

```
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="0",], pairwise.wilcox.test(Mortality, Trt, p.adj = '
bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont   T1
T1 0.0065 -
T2 0.0065 1.0000

P value adjustment method: bonferroni
> with(Mort1[Mort1$Day=="7",], pairwise.wilcox.test(Mortality, Trt, p.adj = '
bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 0.13 -
T2 0.20 1.00

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="10",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 0.93 -
```

```
T2 0.68 1.00

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Mort1[Mort1$Day=="11",], pairwise.wilcox.test(Mortality, Trt, p.adj =
'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Mortality and Trt

   Cont T1
T1 1    -
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties

> Forag1<-read.csv(file='C:/Users/mniesen/Documents/Rwork/Tunnel/EUForaging.c
sv', header=TRUE)
> with(Forag1, tapply(Foraging, Day, shapiro.test))
$`0DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.90808, p-value = 0.07958


$`0DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93925, p-value = 0.2813


$`1DAA`

        Shapiro-Wilk normality test
```

```
data:  X[[i]]
W = 0.95951, p-value = 0.5922


$`1DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94187, p-value = 0.3119


$`2DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.95739, p-value = 0.5521


$`2DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93585, p-value = 0.2458


$`3DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.95614, p-value = 0.5291


$`3DBA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.80158, p-value = 0.001599


$`4DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.91326, p-value = 0.09822
```

```
$`5DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.28046, p-value = 1.633e-08


$`6DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.95334, p-value = 0.4798


$`7DAA`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.921, p-value = 0.1347

> bartlett.test(Foraging[Day=="0DBA"] ~ Trt[Day=="0DBA"], Forag1)

        Bartlett test of homogeneity of variances

data:  Foraging[Day == "0DBA"] by Trt[Day == "0DBA"]
Bartlett's K-squared = 1.9237, df = 2, p-value = 0.3822

> bartlett.test(Foraging[Day=="0DAA"] ~ Trt[Day=="0DAA"], Forag1)

        Bartlett test of homogeneity of variances

data:  Foraging[Day == "0DAA"] by Trt[Day == "0DAA"]
Bartlett's K-squared = 1.7101, df = 2, p-value = 0.4253

> bartlett.test(Foraging[Day=="1DAA"] ~ Trt[Day=="1DAA"], Forag1)

        Bartlett test of homogeneity of variances

data:  Foraging[Day == "1DAA"] by Trt[Day == "1DAA"]
Bartlett's K-squared = 0.58664, df = 2, p-value = 0.7458

> bartlett.test(Foraging[Day=="2DAA"] ~ Trt[Day=="2DAA"], Forag1)

        Bartlett test of homogeneity of variances

data:  Foraging[Day == "2DAA"] by Trt[Day == "2DAA"]
Bartlett's K-squared = 0.53791, df = 2, p-value = 0.7642
```

```
> bartlett.test(Foraging[Day=="3DAA"] ~ Trt[Day=="3DAA"], Forag1)

        Bartlett test of homogeneity of variances

data:  Foraging[Day == "3DAA"] by Trt[Day == "3DAA"]
Bartlett's K-squared = 7.0287, df = 2, p-value = 0.02977

> bartlett.test(Foraging[Day=="4DAA"] ~ Trt[Day=="4DAA"], Forag1)

        Bartlett test of homogeneity of variances

data:  Foraging[Day == "4DAA"] by Trt[Day == "4DAA"]
Bartlett's K-squared = 3.2689, df = 2, p-value = 0.1951

> bartlett.test(Foraging[Day=="5DAA"] ~ Trt[Day=="5DAA"], Forag1)

        Bartlett test of homogeneity of variances

data:  Foraging[Day == "5DAA"] by Trt[Day == "5DAA"]
Bartlett's K-squared = Inf, df = 2, p-value < 2.2e-16

> bartlett.test(Foraging[Day=="6DAA"] ~ Trt[Day=="6DAA"], Forag1)

        Bartlett test of homogeneity of variances

data:  Foraging[Day == "6DAA"] by Trt[Day == "6DAA"]
Bartlett's K-squared = 1.1452, df = 2, p-value = 0.5641

> bartlett.test(Foraging[Day=="7DAA"] ~ Trt[Day=="7DAA"], Forag1)

        Bartlett test of homogeneity of variances

data:  Foraging[Day == "7DAA"] by Trt[Day == "7DAA"]
Bartlett's K-squared = 1.652, df = 2, p-value = 0.4378

> with(Forag1[Forag1$Day=="0DBA",], DunnettTest(Foraging~Trt))#sig T2

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci     upr.ci   pval
T1-Cont  -8.683333 -17.55902  0.1923582 0.0552 .
T2-Cont -15.300000 -24.17569 -6.4243085 0.0015 **

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag1[Forag1$Day=="0DAA",], DunnettTest(Foraging~Trt))#sig all
```

```
  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci     upr.ci    pval
T1-Cont -13.49667 -18.05087  -8.942459 5.7e-06 ***
T2-Cont -15.63000 -20.18421 -11.075793 9.5e-07 ***

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag1[Forag1$Day=="1DAA",], DunnettTest(Foraging~Trt))#sig t2

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci    upr.ci    pval
T1-Cont  -5.05000 -11.71947  1.619467 0.14701
T2-Cont -12.51667 -19.18613 -5.847200 0.00069 ***

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag1[Forag1$Day=="2DAA",], DunnettTest(Foraging~Trt))#Sig t2

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci     upr.ci   pval
T1-Cont -7.066667 -14.77398  0.6406501 0.0732 .
T2-Cont -8.883333 -16.59065 -1.1760165 0.0242 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag1[Forag1$Day=="4DAA",], DunnettTest(Foraging~Trt))#Sig t1

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
              diff    lwr.ci   upr.ci   pval
T1-Cont  5.6666667  1.567405 9.765929 0.0078 **
T2-Cont -0.3833333 -4.482595 3.715929 0.9627

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag1[Forag1$Day=="6DAA",], DunnettTest(Foraging~Trt))#Sig all
```

```
  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff    lwr.ci     upr.ci   pval
T1-Cont -4.283333 -7.622773 -0.9438934 0.0128 *
T2-Cont -5.383333 -8.722773 -2.0438934 0.0025 **

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag1[Forag1$Day=="7DAA",], DunnettTest(Foraging~Trt))#sig T2

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Cont
             diff     lwr.ci     upr.ci   pval
T1-Cont  0.200000  -7.093817  7.4938166 0.9967
T2-Cont -7.883333 -15.177150 -0.5895167 0.0341 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Forag1[Forag1$Day=="3DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Foraging and Trt

   Cont T1
T1 0.20 -
T2 0.28 1.00

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Forag1[Forag1$Day=="5DAA",], pairwise.wilcox.test(Foraging, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  Foraging and Trt

   Cont T1
T1 1    -
```

```
T2 1    1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties

> with(Brood1T1, tapply(BIegg, Day, shapiro.test))
$`14D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.8382, p-value = 0.005547


$`20D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.83709, p-value = 0.005334


$`3D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.86088, p-value = 0.01263


$`8D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.84184, p-value = 0.006313


> with(Brood1T1, tapply(CIegg, Day, shapiro.test))
$`14D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.94456, p-value = 0.3461
```

```
$`20D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96656, p-value = 0.731


$`3D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.91013, p-value = 0.08649


$`8D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.92627, p-value = 0.1669


> with(Brood1T1, tapply(TRegg, Day, shapiro.test))
$`14D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.83807, p-value = 0.005523


$`20D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.83756, p-value = 0.005424


$`3D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.87364, p-value = 0.02044
```

```
$`8D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.84182, p-value = 0.00631


> bartlett.test(CIegg[Day=="20D"] ~ Trt[Day=="20D"], Brood1T1)

        Bartlett test of homogeneity of variances

data:  CIegg[Day == "20D"] by Trt[Day == "20D"]
Bartlett's K-squared = 0.1416, df = 2, p-value = 0.9316

> bartlett.test(CIegg[Day=="14D"] ~ Trt[Day=="14D"], Brood1T1)

        Bartlett test of homogeneity of variances

data:  CIegg[Day == "14D"] by Trt[Day == "14D"]
Bartlett's K-squared = 0.31593, df = 2, p-value = 0.8539

> bartlett.test(CIegg[Day=="3D"] ~ Trt[Day=="3D"], Brood1T1)

        Bartlett test of homogeneity of variances

data:  CIegg[Day == "3D"] by Trt[Day == "3D"]
Bartlett's K-squared = 0.47879, df = 2, p-value = 0.7871

> bartlett.test(CIegg[Day=="8D"] ~ Trt[Day=="8D"], Brood1T1)

        Bartlett test of homogeneity of variances

data:  CIegg[Day == "8D"] by Trt[Day == "8D"]
Bartlett's K-squared = 0.14474, df = 2, p-value = 0.9302

> DunnettTest(CIegg~Trt, data=Brood1T1[Brood1T1$Day=='20D',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
                   diff    lwr.ci   upr.ci   pval
TRT1-Control  0.01666667 -1.397200 1.430534 0.9994
TRT2-Control -0.19500000 -1.608867 1.218867 0.9213

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(CIegg~Trt, data=Brood1T1[Brood1T1$Day=='14D',])
```

```
  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
                    diff    lwr.ci   upr.ci   pval
TRT1-Control  0.17666667 -1.306292 1.659625 0.9404
TRT2-Control -0.08666667 -1.569625 1.396292 0.9852

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(CIegg~Trt, data=Brood1T1[Brood1T1$Day=='3D',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
                   diff    lwr.ci   upr.ci   pval
TRT1-Control 0.1533333 -1.054761 1.361428 0.9328
TRT2-Control 0.1233333 -1.084761 1.331428 0.9558

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(CIegg~Trt, data=Brood1T1[Brood1T1$Day=='8D',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
                    diff    lwr.ci   upr.ci   pval
TRT1-Control  0.19500000 -1.478049 1.868049 0.9429
TRT2-Control -0.01166667 -1.684716 1.661382 0.9998

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Brood1T1[Brood1T1$Day=="20D",], pairwise.wilcox.test(TRegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  TRegg and Trt

     Control TRT1
TRT1 1       -
TRT2 1       1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
```

```
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Brood1T1[Brood1T1$Day=="14D",], pairwise.wilcox.test(TRegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  TRegg and Trt

     Control TRT1
TRT1 1       -
TRT2 1       1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Brood1T1[Brood1T1$Day=="3D",], pairwise.wilcox.test(TRegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  TRegg and Trt

     Control TRT1
TRT1 1       -
TRT2 1       1

P value adjustment method: bonferroni
> with(Brood1T1[Brood1T1$Day=="8D",], pairwise.wilcox.test(TRegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  TRegg and Trt

     Control TRT1
TRT1 1       -
TRT2 1       1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
```

```
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Brood1T1[Brood1T1$Day=="20D",], pairwise.wilcox.test(BIegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  BIegg and Trt

     Control TRT1
TRT1 1       -
TRT2 1       1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Brood1T1[Brood1T1$Day=="14D",], pairwise.wilcox.test(BIegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  BIegg and Trt

     Control TRT1
TRT1 1       -
TRT2 1       1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Brood1T1[Brood1T1$Day=="3D",], pairwise.wilcox.test(BIegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  BIegg and Trt

     Control TRT1
TRT1 1       -
```

```
TRT2 1       1

P value adjustment method: bonferroni
Warning message:
In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Brood1T1[Brood1T1$Day=="8D",], pairwise.wilcox.test(BIegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  BIegg and Trt

     Control TRT1
TRT1 1       -
TRT2 1       1

P value adjustment method: bonferroni
Warning messages:
1: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
2: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
3: In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Brood2T1, tapply(BIegg, Day, shapiro.test))
$`20D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.97793, p-value = 0.9261


$`24D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93179, p-value = 0.2088


$`31D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93163, p-value = 0.2074


$`35D`
```

```
        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.88299, p-value = 0.02932


> with(Brood2T1, tapply(CIegg, Day, shapiro.test))
$`20D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.99202, p-value = 0.9998


$`24D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93488, p-value = 0.2364


$`31D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93813, p-value = 0.2692


$`35D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.96849, p-value = 0.7689


> with(Brood2T1, tapply(TRegg, Day, shapiro.test))
$`20D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.90294, p-value = 0.06467


$`24D`
```

```
        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.93152, p-value = 0.2065


$`31D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.88662, p-value = 0.03379


$`35D`

        Shapiro-Wilk normality test

data:  X[[i]]
W = 0.87861, p-value = 0.02474

> bartlett.test(BIegg[Day=="20D"] ~ Trt[Day=="20D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  BIegg[Day == "20D"] by Trt[Day == "20D"]
Bartlett's K-squared = 2.3029, df = 2, p-value = 0.3162

> bartlett.test(BIegg[Day=="24D"] ~ Trt[Day=="24D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  BIegg[Day == "24D"] by Trt[Day == "24D"]
Bartlett's K-squared = 0.40905, df = 2, p-value = 0.815

> bartlett.test(BIegg[Day=="31D"] ~ Trt[Day=="31D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  BIegg[Day == "31D"] by Trt[Day == "31D"]
Bartlett's K-squared = 1.331, df = 2, p-value = 0.514

> bartlett.test(BIegg[Day=="35D"] ~ Trt[Day=="35D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  BIegg[Day == "35D"] by Trt[Day == "35D"]
Bartlett's K-squared = 0.48642, df = 2, p-value = 0.7841

> bartlett.test(CIegg[Day=="20D"] ~ Trt[Day=="20D"], Brood2T1)
```

```
        Bartlett test of homogeneity of variances

data:  CIegg[Day == "20D"] by Trt[Day == "20D"]
Bartlett's K-squared = 3.4882, df = 2, p-value = 0.1748

> bartlett.test(CIegg[Day=="24D"] ~ Trt[Day=="24D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  CIegg[Day == "24D"] by Trt[Day == "24D"]
Bartlett's K-squared = 0.40528, df = 2, p-value = 0.8166

> bartlett.test(CIegg[Day=="31D"] ~ Trt[Day=="31D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  CIegg[Day == "31D"] by Trt[Day == "31D"]
Bartlett's K-squared = 1.8149, df = 2, p-value = 0.4036

> bartlett.test(CIegg[Day=="35D"] ~ Trt[Day=="35D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  CIegg[Day == "35D"] by Trt[Day == "35D"]
Bartlett's K-squared = 1.3692, df = 2, p-value = 0.5043

>
> bartlett.test(TRegg[Day=="20D"] ~ Trt[Day=="20D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  TRegg[Day == "20D"] by Trt[Day == "20D"]
Bartlett's K-squared = 0.39757, df = 2, p-value = 0.8197

> bartlett.test(TRegg[Day=="24D"] ~ Trt[Day=="24D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  TRegg[Day == "24D"] by Trt[Day == "24D"]
Bartlett's K-squared = 0.38889, df = 2, p-value = 0.8233

> bartlett.test(TRegg[Day=="31D"] ~ Trt[Day=="31D"], Brood2T1)

        Bartlett test of homogeneity of variances

data:  TRegg[Day == "31D"] by Trt[Day == "31D"]
Bartlett's K-squared = 0.25454, df = 2, p-value = 0.8805

> bartlett.test(TRegg[Day=="35D"] ~ Trt[Day=="35D"], Brood2T1)

        Bartlett test of homogeneity of variances
```

```
data:  TRegg[Day == "35D"] by Trt[Day == "35D"]
Bartlett's K-squared = 0.68873, df = 2, p-value = 0.7087

> DunnettTest(BIegg~Trt, data=Brood2T1[Brood2T1$Day=='20D',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
                   diff     lwr.ci    upr.ci   pval
TRT1-Control -0.0300000 -0.3802563 0.3202563 0.9686
TRT2-Control  0.1433333 -0.2069230 0.4935896 0.5185

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(BIegg~Trt, data=Brood2T1[Brood2T1$Day=='21D',])
Error in DunnettTest.default(numeric(0), integer(0)) :
  all observations are in the same group
> DunnettTest(BIegg~Trt, data=Brood2T1[Brood2T1$Day=='31D',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
                  diff     lwr.ci    upr.ci   pval
TRT1-Control 0.0650000 -0.3708264 0.5008264 0.9088
TRT2-Control 0.1066667 -0.3291597 0.5424931 0.7783

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(CIegg~Trt, data=Brood2T1[Brood2T1$Day=='20D',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
                  diff     lwr.ci    upr.ci   pval
TRT1-Control 0.1400000 -0.2430443 0.5230443 0.5864
TRT2-Control 0.1433333 -0.2397109 0.5263776 0.5726

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(CIegg~Trt, data=Brood2T1[Brood2T1$Day=='21D',])
Error in DunnettTest.default(numeric(0), integer(0)) :
  all observations are in the same group
> DunnettTest(CIegg~Trt, data=Brood2T1[Brood2T1$Day=='31D',])
```

```
  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
                   diff     lwr.ci   upr.ci   pval
TRT1-Control 0.03833333 -0.3618954 0.438562 0.9609
TRT2-Control 0.07833333 -0.3218954 0.478562 0.8498

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(CIegg~Trt, data=Brood2T1[Brood2T1$Day=='34D',])
Error in DunnettTest.default(numeric(0), integer(0)) :
  all observations are in the same group
> DunnettTest(TRegg~Trt, data=Brood2T1[Brood2T1$Day=='20D',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
                  diff    lwr.ci   upr.ci   pval
TRT1-Control -3.221667 -11.58551 5.142178 0.5555
TRT2-Control -4.203333 -12.56718 4.160511 0.3868

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> DunnettTest(TRegg~Trt, data=Brood2T1[Brood2T1$Day=='24D',])

  Dunnett's test for comparing several treatments with a control :
    95% family-wise confidence level

$Control
               diff    lwr.ci   upr.ci   pval
TRT1-Control -3.815 -12.42577 4.795773 0.4684
TRT2-Control -3.645 -12.25577 4.965773 0.4974

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> with(Brood2T1[Brood2T1$Day=="35D",], pairwise.wilcox.test(BIegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  BIegg and Trt

     Control TRT1
TRT1 0.16    -
TRT2 0.54    1.00
```

```
P value adjustment method: bonferroni
Warning message:
In wilcox.test.default(xi, xj, paired = paired, ...) :
  cannot compute exact p-value with ties
> with(Brood2T1[Brood2T1$Day=="31D",], pairwise.wilcox.test(TRegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  TRegg and Trt

     Control TRT1
TRT1 0.54    -
TRT2 1.00    1.00

P value adjustment method: bonferroni
> with(Brood2T1[Brood2T1$Day=="35D",], pairwise.wilcox.test(TRegg, Trt, p.adj
= 'bonf'))

        Pairwise comparisons using Wilcoxon rank sum test

data:  TRegg and Trt

     Control TRT1
TRT1 0.40    -
TRT2 0.54    1.00

P value adjustment method: bonferroni
```

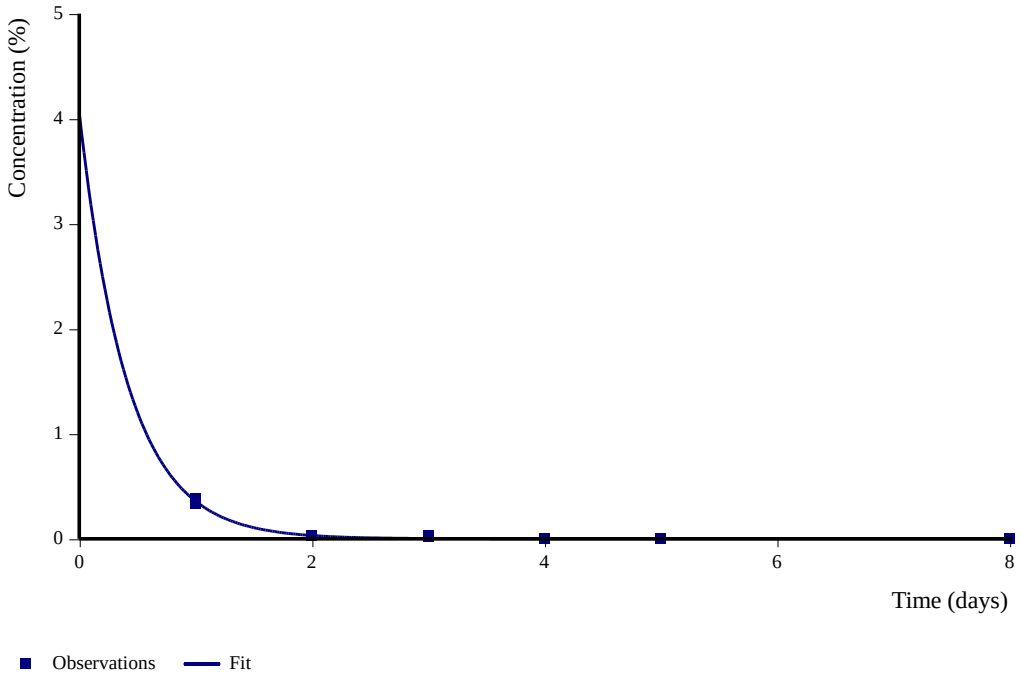
APPENDIX B

CAKE Kinetic Evaluation Report

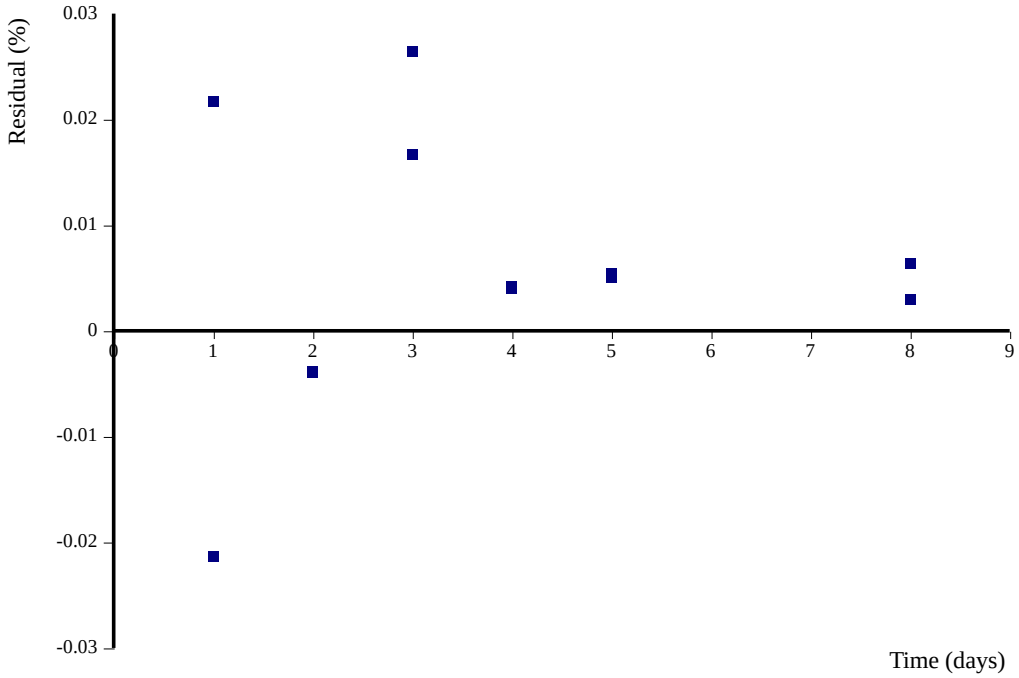
Data set: Phacelia_Nectar_0.022ai/A (SFO)

Graphical Summary:

Observations and Fitted Model:



Residuals:



Initial Values for this Step:

Parameter	Initial Value	Bounds	Fixed
Parent_0	100	0 to (unbounded)	No
k_Parent	0.1	0 to (unbounded)	No

Estimated Values:

Parameter	Value	σ	Prob. > t	Lower (90%) CI	Upper (90%) CI	Lower (95%) CI	Upper (95%) CI
Parent_0	4.055	1.302	N/A	1.695	6.415	1.154	6.956
k_Parent	2.426	0.3174	8.74E-006	1.851	3.002	1.719	3.133

χ^2

Parameter	Error %	Degrees of Freedom
All data	10.7	4
Parent	10.7	4

Decay Times:

Compartment	DT50 (days)	DT90 (days)
Parent	0.286	0.949

Additional Statistics:

Parameter	r^2 (Obs v Pred)	Efficiency
All data	0.9918	0.9897
Parent	0.9918	0.9897

Parameter Correlation:

	Parent_0	k_Parent
Parent_0	1	0.9961
k_Parent	0.9961	1

Observed v. Predicted:

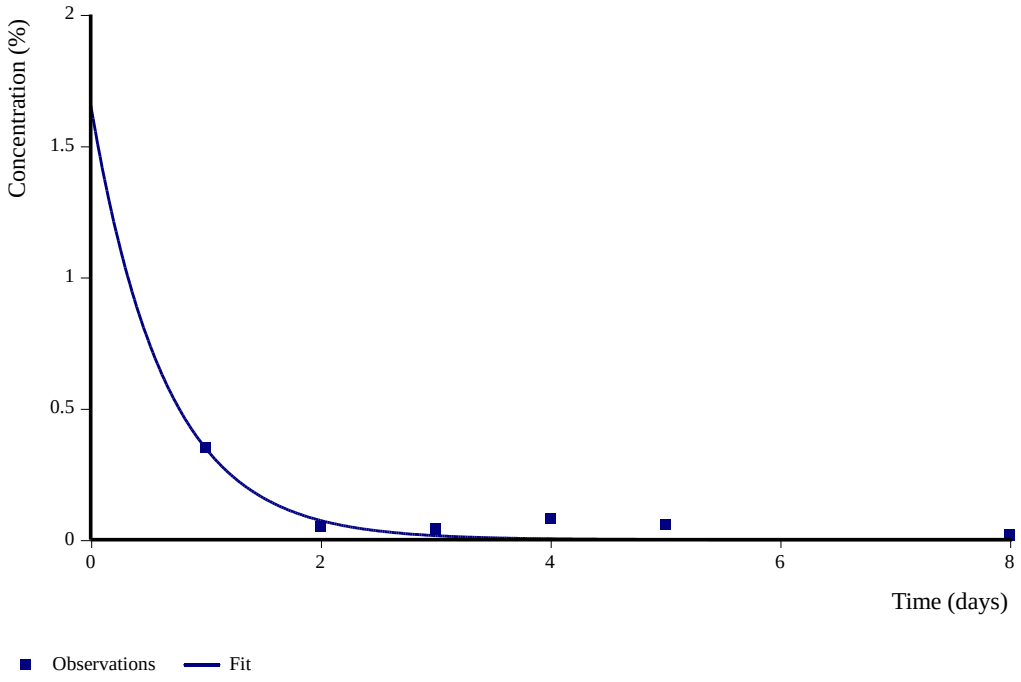
Compartment Parent

Time (days)	Value (%)	Predicted Value	Residual
1	0.337	0.3583	-0.02133
1	0.38	0.3583	0.02167
2	0.0277	0.03166	-0.003964
2	0.0278	0.03166	-0.003864
3	0.0195	0.002798	0.0167
3	0.0292	0.002798	0.0264
4	0.00428	0.000248	0.004032
4	0.00445	0.000248	0.004202
5	0.00501	2.107E-05	0.004989
5	0.00539	2.107E-05	0.005369
8	0.00634	0	0.00634
8	0.003	0	0.003

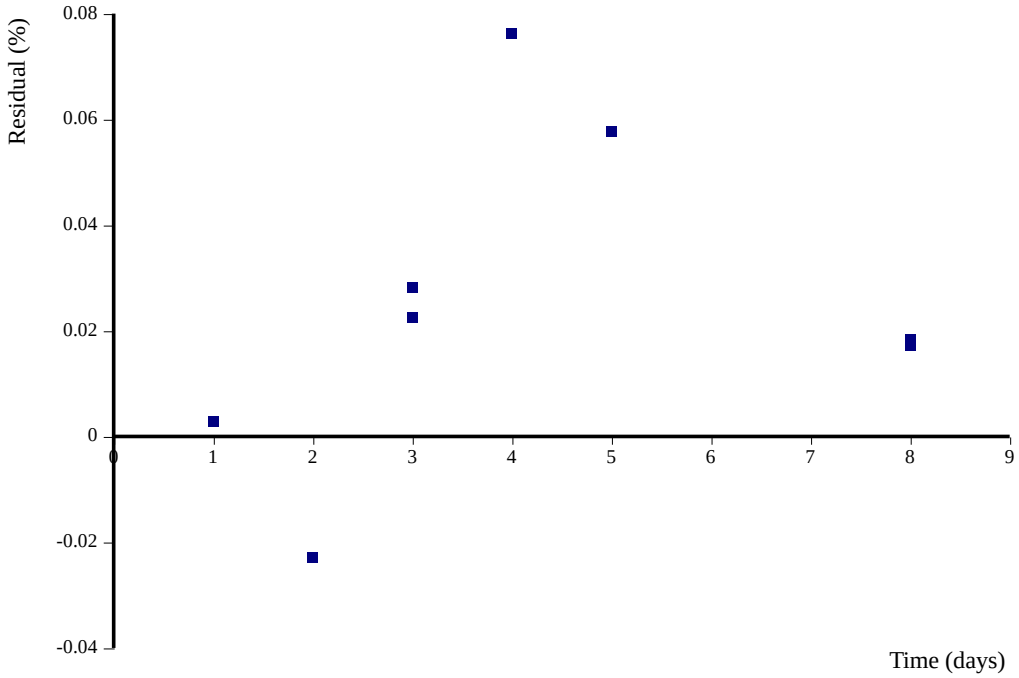
Data set: Phacelia_Pollen_0.022ai/A (SFO)

Graphical Summary:

Observations and Fitted Model:



Residuals:



Initial Values for this Step:

Parameter	Initial Value	Bounds	Fixed
Parent_0	100	0 to (unbounded)	No
k_Parent	0.1	0 to (unbounded)	No

Estimated Values:

Parameter	Value	σ	Prob. > t	Lower (90%) CI	Upper (90%) CI	Lower (95%) CI	Upper (95%) CI
Parent_0	1.654	0.7354	N/A	0.3216	2.987	0.01586	3.293
k_Parent	1.559	0.4159	0.001899	0.8049	2.312	0.632	2.485

χ^2

Parameter	Error %	Degrees of Freedom
All data	33.6	4
Parent	33.6	4

Decay Times:

Compartment	DT50 (days)	DT90 (days)
Parent	0.445	1.48

Additional Statistics:

Parameter	r^2 (Obs v Pred)	Efficiency
All data	0.9342	0.8633
Parent	0.9342	0.8633

Parameter Correlation:

	Parent_0	k_Parent
Parent_0	1	0.9785
k_Parent	0.9785	1

Observed v. Predicted:

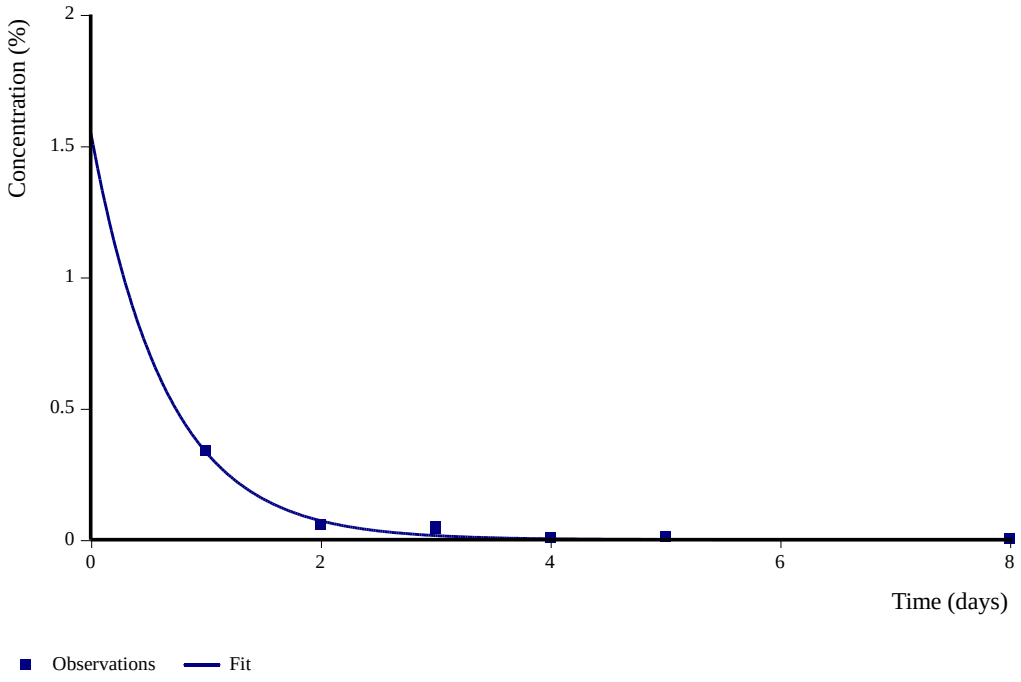
Compartment Parent

Time (days)	Value (%)	Predicted Value	Residual
1	0.351	0.3481	0.002882
1	0.351	0.3481	0.002882
2	0.0503	0.07326	-0.02296
2	0.0503	0.07326	-0.02296
3	0.038	0.01542	0.02258
3	0.0437	0.01542	0.02828
4	0.0795	0.003243	0.07626
4	0.0795	0.003243	0.07626
5	0.0583	0.0006821	0.05762
5	0.0583	0.0006821	0.05762
8	0.0184	0	0.0184
8	0.0173	0	0.0173

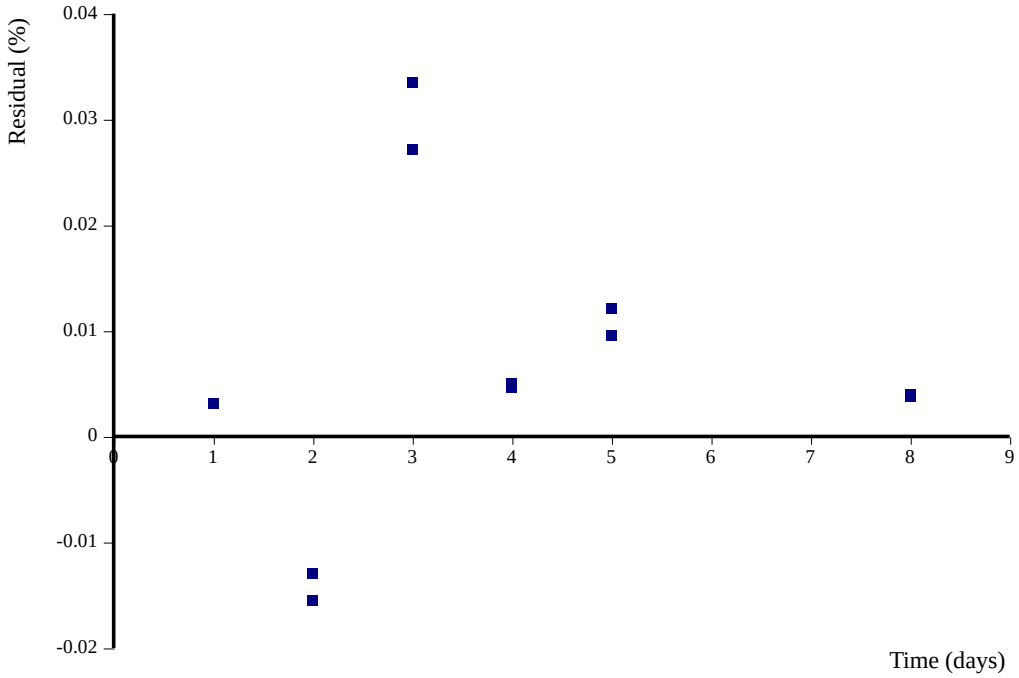
Data set: Phacelia_Nectar_0.042ai/A (SFO)

Graphical Summary:

Observations and Fitted Model:



Residuals:



Initial Values for this Step:

Parameter	Initial Value	Bounds	Fixed
Parent_0	100	0 to (unbounded)	No
k_Parent	0.1	0 to (unbounded)	No

Estimated Values:

Parameter	Value	σ	Prob. > t	Lower (90%) CI	Upper (90%) CI	Lower (95%) CI	Upper (95%) CI
Parent_0	1.551	0.278	N/A	1.041	2.06	0.9219	2.18
k_Parent	1.533	0.1579	2.29E-006	1.243	1.822	1.176	1.89

χ^2

Parameter	Error %	Degrees of Freedom
All data	15	4
Parent	15	4

Decay Times:

Compartment	DT50 (days)	DT90 (days)
Parent	0.452	1.5

Additional Statistics:

Parameter	r^2 (Obs v Pred)	Efficiency
All data	0.979	0.9723
Parent	0.979	0.9723

Parameter Correlation:

	Parent_0	k_Parent
Parent_0	1	0.9629
k_Parent	0.9629	1

Observed v. Predicted:

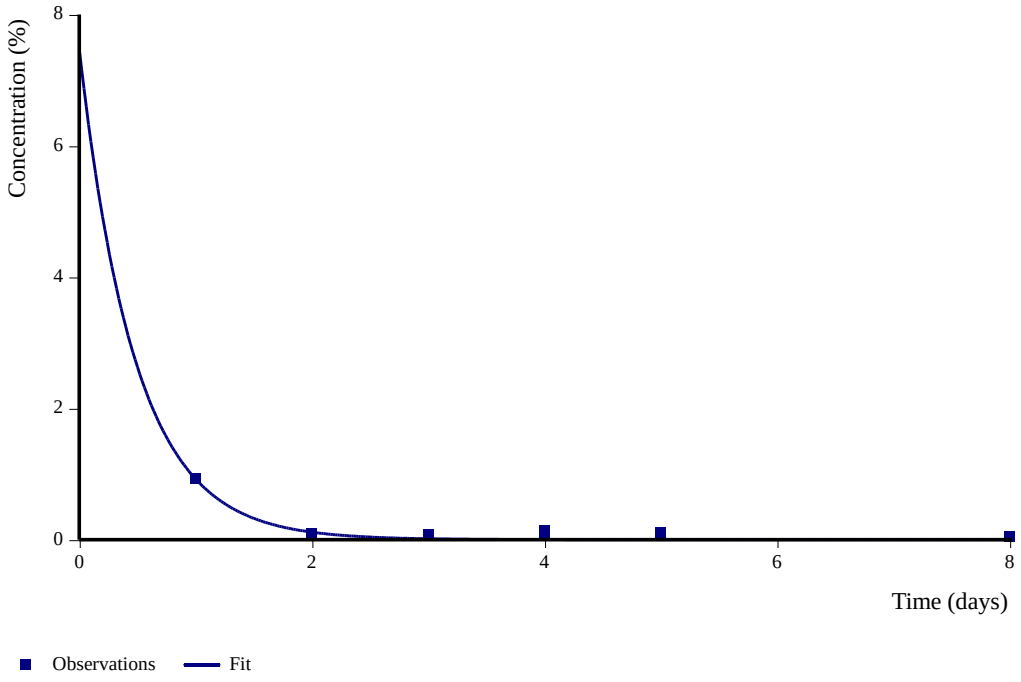
Compartment Parent

Time (days)	Value (%)	Predicted Value	Residual
1	0.338	0.3348	0.003166
2	0.0568	0.07231	-0.01551
2	0.0594	0.07231	-0.01291
3	0.0428	0.01561	0.02719
3	0.0491	0.01561	0.03349
4	0.00799	0.003371	0.004619
4	0.00839	0.003371	0.005019
5	0.0103	0.0007272	0.009573
5	0.0128	0.0007272	0.01207
8	0.00377	0	0.00377
8	0.00401	0	0.00401

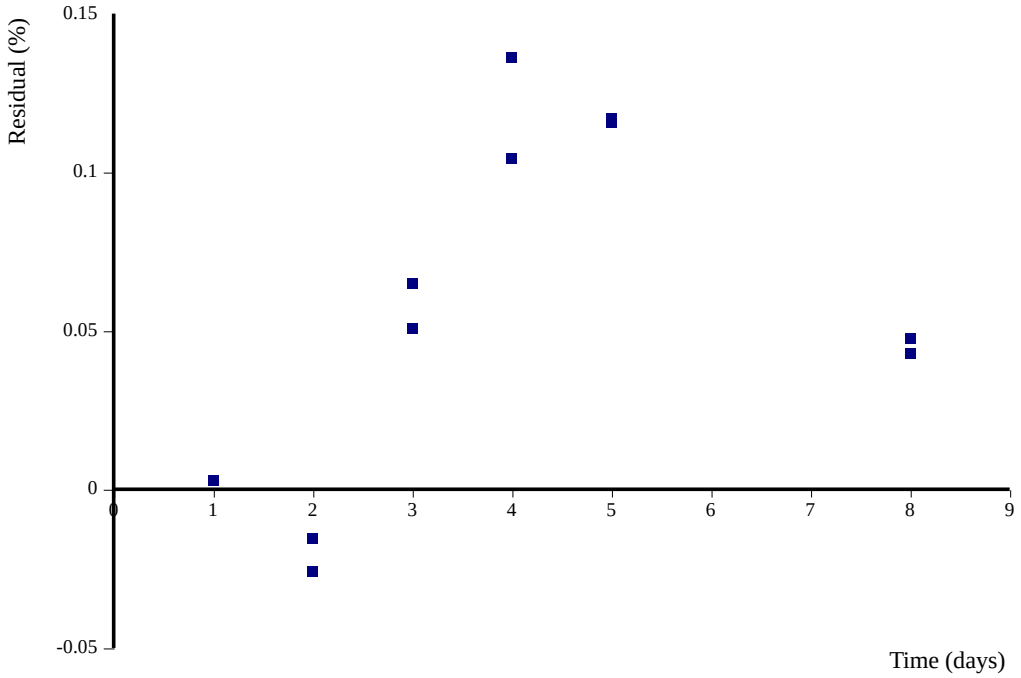
Data set: Phacelia_Pollen_0.042ai/A (SFO)

Graphical Summary:

Observations and Fitted Model:



Residuals:



Initial Values for this Step:

Parameter	Initial Value	Bounds	Fixed
Parent_0	100	0 to (unbounded)	No
k_Parent	0.1	0 to (unbounded)	No

Estimated Values:

Parameter	Value	σ	Prob. > t	Lower (90%) CI	Upper (90%) CI	Lower (95%) CI	Upper (95%) CI
Parent_0	7.473	4.135	N/A	-0.1073	15.05	-1.881	16.83
k_Parent	2.089	0.5293	0.001685	1.119	3.059	0.8917	3.286

χ^2

Parameter	Error %	Degrees of Freedom
All data	26	4
Parent	26	4

Decay Times:

Compartment	DT50 (days)	DT90 (days)
Parent	0.332	1.1

Additional Statistics:

Parameter	r^2 (Obs v Pred)	Efficiency
All data	0.9619	0.8945
Parent	0.9619	0.8945

Parameter Correlation:

	Parent_0	k_Parent
Parent_0	1	0.9859
k_Parent	0.9859	1

Observed v. Predicted:

Compartment Parent

Time (days)	Value (%)	Predicted Value	Residual
1	0.928	0.9251	0.002852
2	0.099	0.1145	-0.01554
2	0.0886	0.1145	-0.02594
3	0.0791	0.01418	0.06492
3	0.0649	0.01418	0.05072
4	0.138	0.001755	0.1362
4	0.106	0.001755	0.1042
5	0.117	0.0002186	0.1168
5	0.116	0.0002186	0.1158
8	0.0428	0	0.0428
8	0.0476	0	0.0476

Sequence Creation Information:
Fit generated by CAKE version 3.3 (Release)
running on R version 3.0.0 (2013-04-03)

Report Information:
Report generated by CAKE version 3.3 (Release)
CAKE developed by Tessella Ltd, Abingdon, Oxfordshire, UK, sponsored by Syngenta
Running on .NET version 4.0.30319.42000